## STIC-Biotech/ChemLib

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From:	<i>l</i> .
Sent:	/1
To:	-11 .
Subject:	$\mathcal{W}$

O'Hara, Eileen Friday, March 28, 2003 6:18 PM STIC-Biotech/ChemLib sequence search for 09/803,589

SEARCH REQUEST FORM-SEQUENCE

Examiner: Eileen O'Hara (Room 10E18) Art Unit 1646

Serial Number: 09/803,589

Novel Genes Encoding Proteins Having Prognostic, Diagnostic, Preventive, Therapeutic and Other Uses

McCarthy et al.

Date: 3/28/03 Phone: 308-3312 CM1 10A01 mailbox 10D19

Please search the following:

SEQ ID NOS: 5 and 6 (nucleic acid and encoded protein)

also, 15 consecutive nucleotides of SEQ ID NO: 5

also, 10 consecutive amino acids of SEQ ID NO: 6

in commercial and patent databases.

Please put results on paper.

Thank you!

Eleen B. O Hara CM 1 10A01 mailbox 10D19 703-308-3312 U.S. Patent and Trademark Office Art Unit 1646 eileen.o'hara@uspto.gov

> POINT OF CONTACT: PAUL SCHULWITZ TECHNICAL INFO. SPECIALIST CM1 6B06 TEL. (703) 305-1954

	TYPE OF SEARCH:	VENDOR/COST (where applic.)
Searcher:	NA Sequences:	STN:
Phone:	AA Sequences:	DIALOG:
Location:	Structures:	Questel/Orbit:
Date Picked Up: 4/4	Bibliographic:	DRLink:
Date Completed: '4/14	Litigation:	Lexis/Nexis:
Searcher Prep/Review:	Full text:	Sequence Sys.:
Clerical:	Patent Family:	WWW/Internet:
Online time:	Other:	Other (specify):

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Sequence 98, Appl Sequence 2, Appli Sequence 11, Appl Sequence 112, App Sequence 112, App Sequence 281, App Sequence 281, Appli Sequence 238, Appli Sequence 9, Appli

Sequence Sequence A

Sequence 8, Ap Sequence 8, Ap Sequence 98, 7

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US-08-841-349-18/C
US-08-841-349-18/C
US-08-841-349-18/C
Sequence 18, Application US/08841349B
Patent No. 595594
GENERAL INFORMATION:
APPLICANT: MISHRA, LOPA
TITLE OF INVENTION: GENES CODING PROTEINS FOR EARLY LIVER DEVELOPMENT.
FILE REFERENCE: XX/PA4470US0
CURRENT APPLICATION UNMER: US/08/841,349B
CURRENT FILING DATE: 1997-04-30
NUMBER OF SEQ ID NOS: 18
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: MISARA, NO. 58112731hiko
APPLICANT: MISARA, NO. 78112731hiko
APPLICANT: KONDO, Keiji
APPLICANT: KAJIWARA, Susumu
APPLICANT: VOKOTAMA, Ahihiro
TITLE OF INVENTION: DNA STRANDS USEFUL FOR THE SYNTHESIS OF
TITLE OF INVENTION: XANTHOPHYLLS AND THE PROCESS FOR PRODUCING THE
TITLE OF INVENTION: XANTHOPHYLLS
CORRESPONDENCE ADDRESS:
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; OTHER INFORMATION: For all n's in this sequence, n=(a or g
US-08-841-349-18
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US-08-406-030A-18
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1.9%; Score 19;
Best Local Similarity 100.0%; Pred. No.
Matches 19; Conservative 0; Mismatc
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COMPUTER READABLE FORM:
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ORGANISM: Mus musculus
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1: /cgqn2_6/ptodata/1/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/1/ina/PcTUS_COMB.seq:*
          GenCore version 5.1.4_p5_4578
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-841-349-18
US-08-65-310-3
US-09-335-919-3
US-08-980-832-33
US-08-980-832-30
US-08-544-900-1
US-08-544-900-1
US-09-187-4-1
US-09-292-036-1
US-09-292-036-1
US-09-335-919-7
US-09-335-919-7
US-09-335-919-7
US-09-345-247-11
US-09-445-247-11
US-09-445-247-11
US-09-445-247-11
US-09-445-247-11
US-09-227-357-96
US-09-227-357-96
US-09-227-357-96
US-09-188-930-255
US-09-188-930-251
US-09-188-930-251
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                                                             OM nucleic - nucleic search, using sw model
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Gapop 60.0 , Gapext 60.0
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length: 2000000000
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Score

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Searched:

Title: Perfect score:

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Sequence:

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APPLICANT: MISAWA, No. 61501301hiko
APPLICANT: KANDO, KEJI
APPLICANT: KOMOO, KEJI
APPLICANT: YOKOYAMA, AKIHIRO
TITLE OF INVENTION: XANTHOPHYLLS AND THE PROCESS FOR PRODUCING THE
TITLE OF INVENTION: XANTHOPHYLLS
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: FOLEY & Lardner
STREET: 3000 K Street, N.W., Suite 500
STREET: BOOK STREET: D.C.
STREET: D.C.
COUNTRY: USA
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/335,919
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ore 19; DB 2;
bred. No. 19;
Mismatches 0
                                                                                                          PULGASJETICATION DATA:
APPLICATION NUMBER: US 08/663,310
FILING DATE: 23-SEP-1996
APPLICATION NUMBER: WO PCT/JP94/02220
FILING DATE: 26-DEC-1994
PRIOR APPLICATION NUMBER: WP 6-235917
FILING DATE: 05-SEP-1994
PRIOR APPLICATION NUMBER: JP 6-235917
FILING DATE: D-1994
APPLICATION NUMBER: JP 5-348737
FILING DATE: 27-DEC-1993
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REFERENCE/DOCKET NUMBER: 4941/109
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1.9%; Score 19;
100.0%; Pred. No.
     CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/006,491
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Patent No. 6150130
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Best Local Similarity 100.0%; P
Matches 19; Conservative 0;
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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STRANDEDNESS: doub
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                                                                                               CLASSIFICATION:
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FEATURE:
NAME/KEY:
LOCATION:
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US-09-006-491-3
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APPLICANT: KONDO, Ke111
APPLICANT: KAJIWARA, Susum
APPLICANT: YOKOYAMA, Akiniro
TITLE OF INVENTION: DNA STRANDS USEFUL FOR THE SYNTHESIS OF
TITLE OF INVENTION: XANTHOPHYLLS AND THE PROCESS FOR PRODUCING THE
NUMBER OF SEQUENCES: 12
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19;
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                    COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
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PatentIn Release #1.0, Version #1.30
                                                                                               CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/663,310
FILING DATE: 23-58P-1996
CLLASSIFICATION ATA:
APPLICATION NUMBER: WO PCT/JP94/02220
FILING DATE: 25-DEC-1994
APPLICATION NUMBER: WO PCT/JP94/02220
FILING DATE: 26-DEC-1994
APPLICATION NUMBER: JP 6-235917
FILING DATE: 05-SEP-1994
APPLICATION NUMBER: JP 5-348737
FILING DATE: 27-DEC-1993
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 49441/109
TELECOMMUNICATION INFORMATION:
TELEFAN: (202)672-5399
TELEEX: 904136
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 489 base pairs
TYPER INCLORATION
STRANDENDESS: Gouble
TTHORNATION FOR SEQ ID NO: 3:
TELENT INFORMATION SEC ID NO: 3:
TELENT INFORMATI
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Mismatches
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STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
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COUNTY: USA
ZIP: 2007-5109
ZIP: ADABABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPALALE
OPERATING SYSTEM: PC-DOS/MS-DC
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Patent No. 5972690
GENERAL INFORMATION:
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Floppy disk
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CORRESPONDENCE ADDRESS:
ADDRESSEE: FOLEY & LA
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Best Local Similarity
Matches 19; Conserva
MEDIUM TYPE:
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LOCATION:
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US-08-663-310-3
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APPLICANT: Pasamontes, Luis
APPLICANT: Tsygankov, Yuri
TITLE OF INVENTION: Improved Fermentative Carotenoid Production
FILE REFERENCE: Improved Fermentive Carotenoid
CURRENT APPLICATION NUMBER: US/08/980,832B
CURRENT FILING DATE: 1997-12-01
NUMBER OF SEC ID NOS: 66
SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                 1.9%; Score 19; DB 4; Length 1261;
100.0%; Pred. No. 18;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1, Application US/08544900
Patent No. 5736331
GENERAL INPORMATION:
APPLICANT: Lin, Stanley Li
APPLICANT: Rothofsky, Marnie Lynn
TITLE OF INVENTION: Method for Identifying Nucleic
TITLE OF INVENTION: Acids Encoding c-fos Promoter;
TITLE OF INVENTION: Acids Encoding c-fos Promoter;
NUMBER OF SEQUENCES: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
ADDRESSEE: Schering-Plough Corporation
ADDRESSEE: Patent Department K-6-1 (1990)
STREET: 2000 Galloping Hill Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OPERATIVE SISTEM: MACIOCOME OF S.13

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/544,900
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/272,412
FILING DATE: 8-ULL-1994
ATTORNEY/AGENT INFORMATION:
NAME: Thompson, Paul ARCISTRATION NUMBER: 35,385
REGISTRATION NUMBER: 35,385
REFERENCE/DOCKET NUMBER: OCO439K
TELECOMMUNICATION INFORMATION:
                                Sequence 30, Application US/08980832B
Patent No. 6291204
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Macintosh 7.1
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ZIP: 07033-0530
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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SEQUENCE CHARACTERISTICS:
LENGTH: 1930 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 100.0
Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA
CRGANISM: Alcaligenes PC-1
US-08-980-832-30
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TELEFAX: 908 298 5388
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STRANDEDNESS: double
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CITY: Kenilworth
STATE: New Jersey
     JS-08-980-832-30
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US-08-544-900-1
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; Sequence 33, Application US/08980832B
; Patent No. 6291204
; GENERAL INFORMATION:
; APPLICANT: Pasamontes, Luis
; APPLICANT: TSygamkov, Yuri
; TITLE OF INVENTION: Improved Fermentative Carotenoid
; CURRENT APPLICATION NUMBER: US/08/980,832B
; CURRENT FILING DATE: 1997-12-01
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 33
; LENGTH: 972
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100.0%; Pred. No. 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 1.9%; Score 19; DB 3; Length 489; Best Local Similarity 100.0%; Pred. No. 19; Matches 19; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
PRIOR PALICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/08/663,310
FILING DATE: 23-SEP-1996
APPLICATION NUMBER: WO PCT/JP94/02220
FILING DATE: 26-DEC-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-235917
FILING DATE: 05-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 5-348737
FILING DATE: 27-DEC-1993
ATTORREY/ASERT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 1.9%; Score 19; DB Best Local Similarity 100.0%; Pred. No. 18; Matches 19; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                     REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 49441/109
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 330 GCGGCCGAGGCGCAGGAG 348
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(202)672-5399
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TELEX: 904136
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGIH: 489 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      mat_peptide
1..486
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1..486
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ORGANISM: E-396
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LOCATION:
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US-09-335-919-3
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Gaps

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GENERAL INFORMATION:
APPLICANT: FIBROGEN, INC
APPLICANT: SCHMIND' BILAN
APPLICANT: ALLEN, MATGAZET
APPLICANT: ALLEN, MATGAZET
APPLICANT: ALLEN, MATGAZET
APPLICANT: CARMICHAEL, David
TITLE OF INVENTION: CONNECTIVE TISSUE GROWTH FACTOR (CTGF) AND METHODS OF USE
FILE REFERENCE: FIBROJIO0-1
CURRENT FILING DATE: 1999-104-14
FRIOR APPLICATION NUMBER: US 09/292,036
FRIOR APPLICATION NUMBER: US 09/187,478
FRIOR PILING DATE: 1998-11-06
NUMBER OF SEQ ID NOS: 18
SOFTWARE: PATENTIN VETSION 3.0
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APPLICANT: MISAWA, NO. 78111
APPLICANT: KONDO, Kelj1
APPLICANT: KAJIWARA, Susumu
APPLICANT: YOKOTAMA, Akihiro
TITLE OF INVENTION: NANTHOPHYLLS AND THE PROCESS FOR PRODUCING THE
TITLE OF INVENTION: XANTHOPHYLLS
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
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17;
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: 3000 K Street, N.W., Suite 500
Washington
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100.0%; Pred. No.
:ive 0; Mismatcl
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FILING DATE: 23-SEP-1996
CLASSIFICATION: 435
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                                                                                                                                                        Sequence 1, Application US/09292036
Patent No. 6358741
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; Sequence 7, Application US/08663310; Patent No. 5811273; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-
                         1 GAATTCGGCACGAGGCCAG 19
                                           1 GAATTCGGCACGAGGCCAG 19
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy o
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Matches 19; Conserv
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20007-5109
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Rat
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQ ID NO 1
LENGTH: 2350
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CITY: Wa
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                                                                                                                                      US-09-292-036-1
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                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: Method for Identifying Nucleic Acids Encoding c-fos Promoter P NUMBER OF SEQUENCES: 2
COMPUTER READABLE FORM:
MEDIUM TYPE: Eloppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 7.1
SOFTWARE: Microsoft Word 5.1a
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/07874
FILING DATE: -June-1995
FILING DATE: B-JUL-1994
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISICS:
LENGTH: 1930 base pairs
TYPE: NUCLEI CACH
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APPLICANT: Schmidt, Brian F.
APPLICANT: Schmidt, Brian F.
APPLICANT: Allan, Margaret L.
TITLE OF INVENTION: Connective Tissue Growth (CTGF) And Methods Of Use FILE REFERENCE: 08766/004001
FILE REFERENCE: 19876/004001
CURRENT APPLICANTION NUMBER: US/09/187,478
CURRENT FILING DATE: 1998-11-06
NUMBER OF SEQ ID NOS: 2
SOFTWARE: Patentin Ver. 2.0
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                                                                           Length 1930;
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                                                                                                                  0; Indels
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                                                                             DB 1;
17;
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ORGANISM: No. 6348329mal Rate Kidney Fibroblast
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Pred. No. 17;
0; Mismatches
                                                                                              Pred. No. 17;
Mismatches
                                                                             Score 19;
                                                                                                                                                                                                                                                                 PCT-US95-07874-1; Sequence 1, Application PC/TUS9507874; GENERAL INFORMATION:
APPLICANT:
                                                               1.9%; Scor.
100.0%; Pre
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100.0%; Pre
0;
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Patent No. 6348329
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                                                                         Query Match
Best Local Similarity 100.C
Matches 19; Conservative
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Best Local Similarity 100.0
Matches 19; Conservative
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; LOCATION: (212)..(1252)
US-09-187-478-1
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
US-08-544-900-1
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STRANDEDNESS:
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PCT-US95-07874-1
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US-09-187-478-1
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Gaps
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Patent No. 6150130
GENERAL INFORMATION:
APPLICANT: MISAWA, No. 6150130ihiko
APPLICANT: KONDO, Keiji
APPLICANT: KOMUO, Keiji
APPLICANT: YOKOYAMA, Akihiro
TITLE OF INVENTION: DNA STRANDS USEFUL FOR THE SYNTHESIS OF
TITLE OF INVENTION: XANTHOPHYLLS AND THE PROCESS FOR PRODUCING THE
TITLE OF INVENTION: XANTHOPHYLLS
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1.9%; Score 19; DB 2; Length 2886;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 19; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
APPLICATION NUMBER: US/09/335,919
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CLASSIFICATION:
PRICA REPLICATION DATA:
PRICATION DATA:
PILING DATE: 23-SEP-1996
APPLICATION NUMBER: WO PCT/JP94/02220
FILING DATE: 26-DEC-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WP 6-235917
FILING DATE: 05-SEP-1994
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET: FOLEY & Lardner STREET: 3000 K Street, N.W., Suite 500 CITY: Washington STATE: D.C. COUNTRY: USA
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FILING DATE: 27-DEC-1993
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 49441/109
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
                                                                                                    49441/109
    FILING DATE: 27-DEC-1993
ATTORNEY AGENT INFORMATION:
NAME: BENT, Stephen
REGISTRATION NUMBER: 29,768
REFRENCE/DOCKET NUMBER: 49441
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5309
TELEFAX: (202)672-5399
                                                                                                                                                                                 TELEX: 904136
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 2886 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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                                                                                                                                                                                                                                                                                                                           ; TOPOLOGY: linear
US-09-006-491-7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: MISANA, NO. 5972690ihiko
APPLICANT: KONDO, Keiji
APPLICANT: KAJUMARA, Susumu
APPLICANT: YOKOYAMA, Akihiro
TITLE OF INVENTION: DNA STRANDS USEFUL FOR THE SYNTHESIS OF
TITLE OF INVENTION: XANTHOPHYLLS AND THE PROCESS FOR PRODUCING THE
TITLE OF INVENTION: XANTHOPHYLLS
CORRESPONDENCES: 12
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 2886;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Indels
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ZIP: 20007-5109.

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURREMY APPLICATION DAFA:
APPLICATION NUMBER: US/09/006,491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 1;
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STREET: 3000 K Street, N.W., Suite 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/663,310
FILING DATE: 23-SEP-1996
APPLICATION NUMBER: WO PCT/JP94/02220
FILING DATE: 26-DEC-1994
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/JP94/02220
FILING DATE: 26-DEC-1994
                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 49441/109
TELECOMMUNICATION INFORMATION:
TELEFEN: (202)672-5300
TELEFEN: (202)672-5399
TELEFA: 904124
                                              FILING DATE: 26-DEC-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-235917
FILING DATE: 05-SEP-1994
PRIOR APPLICATION NUMBER: JP 5-348737
FILING DATE: 27-DEC-1993
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 05-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 5-348737
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FILING DATE: 05-SEP-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 7, Application US/09006491 Patent No. 5972690 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1325 GCGGGCCGAGGCGCAGGAG 1343
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 1.9%
Best Local Similarity 100.0
Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                    TELEPHONE: (202)672-53
TELERAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                           nucleic acid
EDNESS: double
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LENGTH: 8310 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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LOCATION: 680..765
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: USA
ZIP: 19477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:

APPLICANT: DECKER, Heinrich
TITLE OF INVENTION: ISOLATION OF THE BIOSYNTHESIS GENES FOR
TITLE OF INVENTION: BEUDO-CLIGOSACCHARIDES FROM STREPTOMYCES GLAUCESCENS
TITLE OF INVENTION: GLA.O AND THEIR USE
NUMBER OF SEQUENCES: 13
CORRESPONDENCES: 13
CORRESPONDENCES: ADADRESS:
ADDRESSEE: FOLEY & LARDNER
STREET: 3000 K Street, N.W.
CITY: Washington
STAPE: D.C.
COUNTRY: U.S.A.
ZIP: 20007-25109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION WUMBER: US/09/194,905
FILING DATE: 29-JUL-1998
CLASSIFICATION NUMBER: US/09/194,905
FILING DATE: 29-JUL-1998
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1.9%; Score 19; DB 3; Length 2886;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 19; Conservative 0; Mismatches 0; Indels
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APPLICATION DATA:
APPLICATION NUMBER: WO PCT/EP97/02826
FILING DATE: 30-MAY-1997
FILING DATE: 30-MAY-1997
FILING DATE: 07-MAY-1996
FILING DATE: 07-MAY-1996
ATTORNEY/AGENT INFORMATION:
NAME: Granados, Patricia D.
RECISTRATION NUMBER: 33,683
REFERENCE/DOCKET NUMBER: 026083/0193
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1.9%; Score 19; DB
100.0%; Pred. No. 15;
tive 0; Mismatches
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Patent No. 6306627
                                                                                                                                                                                                                                                                                                                        1325 GCGGCCGAGGCGCAGGAG 1343
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; MOLECULE TYPE: DNA (genomic) US-09-194-905-7
TELEX: 904136
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                             330 GCGGGCCGAGGCGCAGGAG 348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: (202) 672-5300
TELEPAX: (202) 672-5399
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARATTERISTICS:
LENGTH: 6854 base pairs
                                                                    LENGTH: 2886 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
1 TOPOLOGY: linear
US-09-335-919-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 100.
Matches 19; Conservative
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STRANDEDNESS: single
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Sequence 11. Application US/08870126

Partent No. 60487018

Sequence 11. Application US/08870126

Partent No. 60487018

APPLICANT: Sakamuro, Daltoku

NUMBER OF SOURCES: 14

CORRESS: Howan and Howan

STITE OF INVENTION: WITHIN and Human Box-Dependent

TITLE OF INVENTION: WITHIN and Human Box-Dependent

TITLE OF INVENTION: WITHIN AND HUMBER OF SOURCES: 14

CORRESS: SOURCES: 14

CORRESS: Grain Howan and Howan

STITE: Spring House Corporate Cutr, P O Box 457

STRING SPRING: PORM: WITHIN AND HUMBER OF SOURCES: 14

CORPUTER: BANDALE FORM: WITHIN AND HUMBER: US/08/48-DoS

SOURTHER: BANDALE FORM: WITHIN AND HUMBER: US/08/48-DOS

SOURTHER: BANDALE FORM: WITHIN APPLICATION BANDALE: US/08/48-DOS

CORRESTED STRING: US/08/48-DOS

SOURTHER: BANDALE FORM: US/08/48-DOS

CORRESTED STRING: US/08/48-DOS

TELEBHOWN: US/08/48-DOS

US/ATION: US/08/48-DOS

US/08/48-DOS

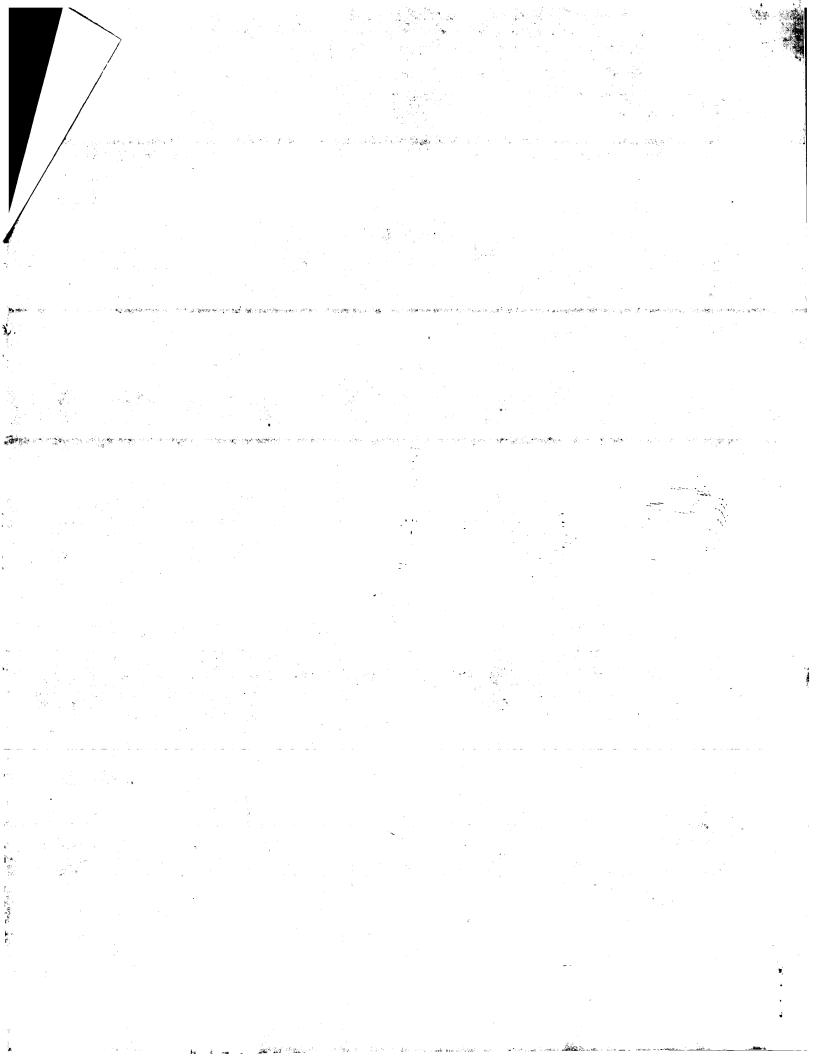
US/08/4
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; NAME/KEY: exon
; LOCATION: 7094..721
; OTHER INFORMATION: /note= "exon 12"
US-08-870-126-11
Query Match 1.9%; Score 19; DB 3; Length 8310;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 19; Conservative 0; Mismatches 0; Indels
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0; Gaps

Search completed: April 12, 2003, 20:48:34 Job time : 139 secs



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April 12, 2003, 19:17:08; Search time 2722 Seconds (without alignments) 10467.174 Million cell updates/sec
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GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
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                                                                                                                                                                                                                                      2054640 seqs, 14551402878 residues
                                                     OM nucleic - nucleic search, using sw model
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Gapop 60.0 , Gapext 60.0
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em_htg_inv:*
em_htg_other:*
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em_htgo_other:*
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em_sy:*
em_htgo_hum:*
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em_htg_pln:*
em_htg_rod:*
em_htg_mam:*
                                                                                                                                                                                                                                                                                                                      Minimum DB seq length: 0 ... Maximum DB seq length: 2000000000
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979
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9b_in:*
9b_on:*
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9b_pat:*
9b_pi:*
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Perfect score:
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                                                                                 Run on:
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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

SUMMARIES ID Descri	orania de la companya	BC002851	AX083428 Sequen	AF181562 Homo s	AX083418 AX083418 Sequen	AF196971 AF196971	AX336215	AA4U9U34 AA4U9U34 O AF181561 AF181561	0 BC012263 BC012263 Mus musc	0 AF293356 Mus mus	0 AF181560 AF181560 Mus mu	ACOVB339 ACOSB473	AC094563 AC094563 Rattus	0 AL670169 Mouse	AC123014 AC123014 Rattus	CHKW4P D31900 Chicken	AP005551 AP005551	AX071185 Sequence	0 AF133100 0 AF064874 AF064874	0 AF332063 Aus mus	0 AF332064 Mus mu	0 AF247453 AF247455	AC115188 AC115188	AC112282	AL646070 AL646070	AC094816	0 AL591495 Mouse	AC093408 AC093408	AB022927	STMSVIDEOX L37334 S	SVI011500 AJ011500	AC103083	AP003964 AP003964 Oryza	AL138781 AL138781 Human	AC103312 ACTUB AC103046 Battus	AC130160 AC130160 Rattu	BIN421636 AJ421636 Bos in	ALIGNMENTS		1	n-like neurcendocrine peptide precursor	our, mkwa, comprete co	4000		Chordata: Craniata: Vertebrata: Euteleostomi:	
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a Query ore Match	E March	91.0	85.8	80.2	69.3	38.3	23.1	3.5	3.6	3,3	m .	. (c	3.6	3,3	m r	7	2.5	2.5	7.0	2.2	2.5	2 .	9 79	2.2	2.5	2.5	2.2	2.5	2.1	2.1	2.7	2.1	2.1	7.7	1.5	21 2.1	2.0			BC002851	2,4	BC002851	BC002851.1	Homo sapie	Homo sapiens Eukarvota: Me	Wamma lia.
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Homo sapiens
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VERSION
KEYWORDS
SOURCE
ORGANISM
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TITLE
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AX083428
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                                                                                                                                                CDNA Library Preparation: Rubin Laboratory
CDNA Library Preparation: Subin Laboratory
CDNA Library Prayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing Dy: National Institutes of Health Intramural
Sequencing Center (NISC),
Gaithersburg, Maryland;
Mtp://www.nisc.nih.gov/
Contact:
Natyland:
Shevchenko,Y., Wetherby,K.D., Beckstrom-Sternberg,S.M.,
Benjamin,B., Blakesley,R.W., Bouffard,G.G., Brinkley,C., Brooks,S.,
Dietrich,N.L., Guan,X., Gupta,J., Ho,S.-L., Karlins,E., Legaspi,R.,
Lim,M., Maduro,G.L., Masiello,C., Mastrian,S.D., McCloskey,J.C.,
McDowell,J., Pearson,R. Snyder,B., Stantripop,S., Thomas,P.J.,
Tlongson,E.E., Touchman,J.W., Tsurgeon,C., Vogt,J.L., Walker,M.A.,
Zhang,L.-H. and Green,E.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                    Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at: http://image.llnl.gov Series: IRAL Plate: 12 Row: n Column: 24 This clone was selected for full length sequencing because it passed the following selection criteria: GenomeScan gene prediction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /translation="MAGSPLLWGPRAGGGGLLVLLLLGLFRPPPALCARPVKEPRGLS
AASPPLAETGAPRRFRRSVPRGEAAGAVQELARALAHLLEAERQERARAEAGEAEDQO
ARVLAQLLRARLDPAALAAGLDDPDAPAAQLARALLRARLDPAALAAQLVPAPVP
ARALRPRPFVYDGFAGPDEEAGDDPDPAPAQLARALLRARLDPAALAAQLVPAPVP
RRAALRPRPFYYDGFAGPAEEAGDETPDVDPELLRYLLGRILAGSADSEGVAAPRRL
RRAALRPPRYSUPGSELPFYKRLETPAPQVPARRLLPP"

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Submitted (05-FEB-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
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/db_xref="GI:12804001"
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/lab_host="DH10B-R"
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Pred. No. 0;
0; Mismatches 1; Indels
                                                                            http://mgc.nc1.nih.gov
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/organism="Homo sapiens"
/db_xref="LocusID:27344"
/db_xref="taxon:9606"
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/codon_start=1
                                                                                        Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
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                                                                            NIH-MGC Project URL:
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Best Local Similarity 99.9%;
Matches 941; Conservative
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Catarrhini; Hominidae; Homo.
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SAGAMI CHEMICAL RESEARCH CENTER (JP) ; Protegene Inc. (JP)
Location/Qualifiers
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/organism="Homo sapiens"
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/protein_id="CAC33311.1"
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Mammalia; Eutheria; Primates;
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Kato,S. and Kimura,T.
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/db_xref-"G1:13185275"
Artanslation="MAGSPLLMCPRAGGVGLLVLLLGLFRPPPALCARPVKEPRGLS
AASPPLAETGAPRKFRSVPKGEAAGAVOELARAHLLEREROBERARAAGBAEDQQ
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AAALRPRPVVDGPAGPAEEAGDETPDVDPELLRYLIGRILAGSADSEGVAAPRRL
RRAAHHVGSELPPEGVLGALLRYKRLETPAPQVPARRLLPP"
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//product="proSAAS"
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Levin, N., Mzhavia, N.,
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Levin, N., Mzhavia, N.,
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Fricker,L., McKinzie,A.A., Sun,J., Curran,E., Qian,Y., Yan,L., Patterson,S.D., Courchesne,P.L., Richards,B., Levin,N., Mzhavia,N. Devi,L.A. and Douglass,J.
Identification and characterization of proSAAS, a granin-like neuroendocrine peptide precursor that inhibits prohormone
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/function="inhibits prohormone processing"
/note="granin-like neuroendocrine peptide precursor"
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Submitted (30-AUG-1999) Department of Molecular Pharmacology,
Albert Einstein College of Medicine, 1300 Morris Park Avenue,
Bronx, NY 10461, USA
Location/Qualifiers
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Fricker,L., McKinzie,A.A., Sun,J., Curran,E.,
Patterson,S.D., Courchesne,P.L., Richards,B.,
Devi,L.A. and Douglass,J.
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="FLHSAAS"
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Homo sapiens GATA-binding protein 1 and histone deacetylase-like protein genes, complete cds; CRAS pseudogene, complete sequence; and protein translocase gene, partial cds.
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SAGAMI CHEMICAL RESEARCH CENTER (JP) ;
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Mammalia; Eutheria; Primates;
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Kato, S. and Kimura, T.
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/evidence=not_experimental /rpt_family="MIR" 5062. :5157 /rote="homology = 67.70%, score = 32, counts = 48" /rote="homology = 67.70%, score = 32, counts = 48" /rote_type=tandem /rpt_type=tandem /rpt_unit=tc 5649. :5691 /evidence=not_experimental	/rpt_family="MIR" 6131. 13747 /gene="GATA-1" join 61316168.1061410852,1136711744,1184611991,	-bindin c. no.	/gene="GATA-1" . /nube=-1 8548 8857	/evidence=not_experimental //Fpt_family="AluSx"	/eviden.ce-not_experimental /rpt_family="AluJb"		join(1063310852,1136711744,1184611991,1269512820, 1331613687) /gene="GATA-1"	/note="globin transcription factor 1; GF-1" /codon_start=1 /broduct="GATA-binding protein 1"	/protein_id="AAF06806.1" /b_xref="(1:6289081" /+aaola+iva="Areborner.org	ASSTARSTATAMAALAYYENDOODALEETEY VERMAYOO ELOOTETSATEADALAYYENDOODALEETEY TEATAMAALAYYENDOODALEETEY TEATAMAALAYYENDOODALEETEY TEATAMAALAYYENDOODALEETEY TEATAMAALAYYENDOODALEETEY TEATAMAALAYYENDOODALEETEY TEATAMAA TATAAA TATAAAA TATAAAA TATAAAA TATAAAA TATAAAA TATAAAAA TATAAAAA TATAAAAAA	RTGHYLCNACGLYHKMRQNRPLIRPKRRLIVSKRAGTQCTNCQTTTTTLHRRNASGD PVCNACGLYYKLLHVNRPLIRPKRRLIVSKRAGTQCTNCQTTTTTTTTTTARRNASGD MVUNCCGCCNYCCTVACTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT	AV ANGOSOGNICOS ANGOLI LOS FOI FRILLIGIOS VALGOS VA	/gene="GATA-1" /number=3 118./f 11001		complement(12330, .12477) /evidence-not_experimental	/rpt_ramily="MERSB" 1269512820 /gene="GATA-1"	//inducers //inducers //gene="GATA-1"	/number=6 14173. 14226 /note="homology = 98.10%, score = 25, counts = 2"	/rpt_type=tandem /rpt_unit=ggcatgacgctggggaccttttagac /rpt_unit=ggcatgacgctggggaccttttagac	comics	<pre>complement(1487614972) /evidence=not_experimental /rpt_family="MIR"</pre>
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 113853) Blechschmidt, K., Myakatura, G., Strom, T.M., Drescher, B., Menzel, U., Meindl, A. and Rosenthal, A. Direct Submission Submitted (14-OCT-1999) Genome Analysis, Institute of Molecular Blotecthology, Beutenbergstrasse 11, Jena 07745, Germany 1-3652: cosmid 11045; 11106-52106: cosmid E2237, 27017-67034: cosmid L1850; 58536-92644: cosmid D1425, 80573-113853: cosmid	ors apiens"	/chromosome="x" /map="xp11.23" /clone="cosmids J1045; E2237; L1850; D1425; E1239" 1252	perimental	perimental 4"	kperimental 1Sg"	xperimental M4"	xperimental vB;"	. 1371) yperimental	xperimental MR7"	Toprimental Mn0"	)2440)  p. prental	0.3059) experimental	IK" pxnarimental	IR"	experimental .uJo"	= 80.00%, score = 28, counts = 3" xperimental	//rpt_unit-tragcattagaatagttttactattaaaattagta 36133955		<pre>xxperimental multiple</pre>	/evidence=nc_experimental /rpt_family="MIR" 4393 .4463	_experimental 12" 324544)
Mammalia; Eutheria; Primat 1 (bases 1 to 113853) Blechschmidt,K., Nyakatura Meindi,A. and Rosenthal,A. Direct Submission Submitted (14-OCT-1999) Ge Botechnology, Beutenbergs 1-36552: cosmid JUG5; 111 cosmid L1850; 58536-92644:	Location/Qualifiers 1113853 /organism="Homo sapiens' /db xref="taxon:9606"	/chromosome="x" /map="xp11.23" /clone="cosmids J1045; E2237 1252	/evidence=not_exp /rpt_family="Alu: 254396	/evidence=not_experimental /rpt_family="LIM4" 397 704	/evidence=not_experimental /rpt_family="AluSg" 705 717	/evidence=not_experimental /rpt_family="L1M4"	<pre>8171083 /evidence=not_e: /rpt_family="L11</pre>	<pre>complement(10841371) /evidence=not_experimental /rpt_family="AluJo"</pre>	13721790 /evidence=not_experimental /rot_familv="f.1MB7"	18021924 /evidence=not_experimental /rnt_familv="1.1MD"	complement(22692440) /evidence=not_experimental /rot_familv="f.2"	complement(295)	/ipt_ramily="Mik" 31053235 /evidence=not experimental	/rpt_family="MIR" 32683472	/evidence=not_experimental /rpt_family="AluJo" 2504	/note="homology /evidence=not_ex /rnt_twne=tander	/rpt_unit=ttages 36133955	/evidence=not_experimental /rpt_family="LiMA5" 39644059	/NOte= nomology = //.lu%, /evidence=not_experimental /rpt_type=tandem /rpt_unit=aataatattagtatta /comolement/4/21 4360	/evidence=not_e /rpt_family="MI 43934463	/evidence=not_experimental /rpt_family="L2" complement(45024544)

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Young, P.E., Augustus, M., Carter, K.C., Ebner, R., Endress, G., Horrigan, S., Soppet, D.R. and Weaver, Z. Cancer gene determination and therapeutic screening using signature gene sets
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Sequence 6724 from Patent WO0194629.
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/db_xref="taxon:9606"
79 c 131 g 46
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Location/Qualifiers
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Best Local Similarity 99.6%;
Matches 276; Conservative
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/rpt_family-"MrII"
complement(18388...1868)
/evidence-not_experimental
/rpt_family-"Alusx"
complement(1864...1877)
/evidence-not_experimental
/rpt_family-"Alusg"
/evidence-not_experimental
/evidence-not_experimental
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/evidence=not_experimental
/rpt_family="MIR"
20598. .20658
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19750. .19923
/evidence=not_experimental
/rpt_family="MER58c"
complement(14989. .15178)
/evidence=not_experimental
/rpt_family="MIR"
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                                                                   16160. 16259
/note="homology = 74.00%,
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/protein_id="AaF22642.1"
/db_xref="G1:6653211"
/translation="MAGSPELCGPRAGGGILVLLLIGLLRLPPTLSARPVKEPRSLS
/translation="MAGSPECAGAGGAGELARALAHLLEAERGERARAGEAEDGG
ARVLAGLLRAMGSPFRASDPPLAPDDPDAAPAQLARALLARALLDPAALAAGLVVBAPAP
AAALRPRPPVYDDGPTGPDVEDAADETPDVDPELLRYLLGRILLTGSSEPEAAPARRL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Web site: http://www.ngsc.bcm.tmc.edu/cdna/
Contact: amg@bcm.tmc.edu A.M., Lu, X., Hulyk, S.W., Hale, S.M.,
Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Hale, S.M.,
Yoon, V.S., Kowis, C.R., Lawrence, S., Martin, R.G., Muzny, D.M.
Richards, S., Gibbs, R.A.
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//tissue_type="Colon, normal. 5 month old male mouse."
//clone_lib="NCI_CGAP_CO24"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                             Gaps
    /note="granin-like neuroendocrine peptide precursor"
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Mus musculus, Similar to granin-like neuroendocrine peptide precursor, clone MGC:19107 IMAGE:4207854, mRNA, complete cds.
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Baylor College of Medicine Human Genome
Sequencing Center
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/db_xref="taxon:10090"
/map="FVB/N"
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                                            /product="proSAAS"
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Mammalia; Eutheria;
1 (bases 1 to 975)
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Direct Submission
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Fricker,L., McKhazie,A.A., Sun,J., Curran,E., Qian,Y., Yan,L., Partkerson,S.D., Courchesne,P.L., Richards,B., Levin,N., Mzhavia,N., Devi,L.A. and Douglass,J. Identification and characterization of proSAAS, a granin-like neuroendocrine peptide precursor that inhibits prohormone
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Fricker,L., McKinzie,A.A., Sun,J., Curran,E., Qian,Y., Yan,L.,
Patterson,S.D., Courchesne,P.L., Richards,B., Levin,N., Mzhavia,N.,
Devi,L.A. and Douglass,J.
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Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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                                                    /organism="Homo sapiens"
/organism="Homo sapiens"
/db_xref="taxon:9606"
/note="EMBL/GenBank Accession No. D59847"
/note="EMBL/GenBank Accession No. D59847"
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AF181561 GI:6653210
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0229103-A 1701 11-APR-2002;
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/organism="Rattus norvegicus"
/db_xref="taxon:10116"
/clone="FLRSAAS"
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20098938
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                  C INC (US)
Location/Qualifiers
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Location/Qualifiers
                                                                                                                                                                                                    23.18;
                                                                                                                                                                                             Query Match
Best Local Similarity 99.69
Matches 276; Conservative
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Rattus norvegicus
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Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bass 1 to 10.27); Fricker, L., McKinzie, A.A., Sun, J., Curran, E., Qian, Y., Yan, L., Patterson, S.D., Courchesne, P.L., Richards, B., Levin, N., Mzhavia, N., Tdentification and Douglass, J.

Tidentification and characterization of proSAAS, a granin-like neuroendocrine peptide precursor that inhibits prohormone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rattus norvegicus clone CH230-2A16, *** SEQUENCING IN PROGRESS ***, AC098339.3 GI:22474728
                                                                                                     ROD 27-JAN-2000
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Levin, N., Mzhavia, N.,
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/protein_id="aaF2561.1"
/db_xref="G1:653209"
/translation="MAGSPLLCGPRAGGVGILVLLLLGLIRLPPTLSARPVKEPRSLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AASAPLVETSTPLRLRRAVPRGEAAGAVQELARALAHLQEAERQERARAEAQEAEDQQ
ARVLAQLLARAWGSPRASDPPLARDDDPDAPAJLALLARARLDPAALAAQLVPRPAA
ARPRPPVYDDGPTGPDVEDAGDETBDVDPELLRYLLGRILTGSSEPEAAPAFRRLRR
SVDQDLGPEVVPDENVLGALLRVKRLENPSPQAPARRLLDP"
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/function="inhibits prohormone processing"
/note="granin-like neuroendocrine peptide precursor"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (30-AUG-1999) Department of Molecular Pharmacology, Albert Einstein College of Medicine, 1300 Morris Park Avenue, Bronx, NY 10461, USA
Location/Qualifiers
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Fricker, L., McKinzie, A.A., Sun, J., Curran, E., Patterson, S.D., Courchesne, P.L., Richards, B., Direct Submission
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100.0%; Pred. No. 0.00023;
ive 0; Mismatches 0;
                                                                                             Mus musculus proSAAS gene, complete cds. AF181560
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  85 TGGGGCAGCATGGCGGGGTCGCCGCTGCTCTG 116
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/db_xref="taxon:10090"
/clone="FIMSAAS"
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Mus musculus
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                                                                       Processiald="Aah12263.1"

/db_xref="G1:15126670"

/db_xref="G1:15126670"

/translation="MACSPLICGPRAGGVGILVLILIGILRLPPTLSARPVKEPRSLS

A/translation="MACSPLICGPRAGGAVQELARALAHILEAERQERARAEAOEAEDQO

ARVLAQLIRAMGSPFRASDPPLAPDDDPAPAAQLARALILRAHILDPAALAAQLYPAPAA

APRPRPPVYDDGPTGPDVEDAGDETEDVDPELLRYLLIGRILTGSSEPEAAAPRRIRR
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Donadel,G., Notkins,A.L. and Lan,M.S.

Direct Submission

Direct Submission

Direct Submission

Institute of Dental Research, 9000 Rockville Pike, Building 30 Room

124, Bethesda, MD 20892, USA

Location/Qualifiers

I. .1025

/organism="Mus musculus"

/db_xref="taxon:10090"
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ARSAPLVETSTPLRLRRAVPRGEAAGAVPGAGARGAGAPGGGRDRNARVLRRRRLRIS
RRNSWRSSCAPGALRVPRTRPLAPDDDPDAPAAQLARALLRARLDPAALGAQLVPAPA
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Donadel,G., Marinos,N., DeSilva,M.G., Lu,J., Notkins,A.L. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Molecular cloning and characterization of a highly basic protein, IA-4, expressed in pancreatic islets and brain Neuroendocrinology 67 (3), 190-196 (1998)
                         /product="Similar to granin-like neuroendocrine peptide precursor"
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pancreatic islets and neuronal cells"
/codon_start=1
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353 c 304 q 145 t
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Mus musculus IA4 mRNA, complete cds.
AF293356
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /product="IA4"
/protein_id="AAG09048.1"
/db_xref="GI:9954416"
                                                                                                                                                                                                                                                                                                                                                                 resescatescesses 80
                                                                                                                                                                                                                                                                                                                                                                                      11 TGGGGCAGCATGCGGGGGTCGCCGCTGCTCTG 42
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                                                                                                                                                                                                                       304 g
                     /codon_start=1
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Mus musculus
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VERSION

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NEUZY,D.M. Addans.C., Adio-Oddola,B.A. All-coman,F.K. Allen,C., Barbaria,J., Benten,J., Bimage,K., Blankenburg,K., Bennin,D., Barbaria,J., Benten,J., Bimage,K., Blankenburg,K., Bennin,D., Burbaria,J., Benten,J., Bimage,K., Blankenburg,K., Bennin,D., Burbaria,J., Benten,J., Brieva,M., Brown,H., Bryant,N.C., Carron,T.C., Burch,P., Burkett,C., Burrell,K.L., Byrd,N.C., Chen,G., Chen
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                                                                                                    Eukaryota; Métazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                        Adams, C., Adio-Oduola, B., Ali-osman, F.R., Allen, C.,
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vector: Plasmid;
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Muzny, D.M., Adams, C.,
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KEYWORDS
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COMMENT

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(see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
NOTE: This is a 'working draft' sequence. It currently consists of 38 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the flnished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                          NOTE: Estimated insert size may differ from sequence length
Assembly program: Phrap; version 0.990329
Consensus quality: 23320 bases at least Q40
Consensus quality: 26055 bases at least Q30
Consensus quality: 27205 bases at least Q30
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Moser, M., Neal, D., Newtson, J., Newtson, N., Nguyen, A., Nguyen, N., Nickerson, E., Nwokenkwo, S., Oguh, M., Okwuonu, G., Oraqunye, N., Oviedo, R., Pace, A., Payton, B., Perer, J., Perez, L., Peters, L., Pickens, R., Pirlus, E., Pu, L. L., Quiles, M., Rer, Y., Rives, M., Rojas, A., Rojubokan, I., Rolfe, M., Ruiz, S., Savery, G., Scherer, S., Soctt, G., Shen, H., Shooshtari, N., Sisson, I., Sodergren, E., Sonalke, T., Sparks, A., Stanley, H., Stone, H., Sutton, A., Svatek, A., Tabor, P., Tamerisa, A., Tamerisa, K., Tang, H., Tansey, J., Taylor, C., Taylor, T., Telfrod, B., Thomas, N., Thomas, N., Wang, S., Ward-Moore, S., Warren, R., Washington, C., Watlington, S., Williams, G., Williamson, A., Wleczyk, R., Wooden, S., Warlington, S., Weinstock, G. and Gibbs, R.
Miner,G., Miner,Z., Mitchell,T., Mohabbat,K., Morgan,M., Morris,S.,
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Worley,K.C.

Direct Submission

Submisted (23-0cT-2001) Human Genome Sequencing Center, Department

Of Molecular and Human Genetics, Baylor College of Medicine, One

Baylor Plaza, Houston, TX 77030, USA

3 (bases 1 to 77876)

Worley,K.C.

Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (31-TUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA On Jul 24, 2002 this sequence version replaced 91:20976551.
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Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
Contact: project Information
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Center clone name: CH230-2J23
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Muzny, D.M., Adams, C., Adio-Oduola, B., Ali-osman, F.R., Allen, C., Alsbrooks, S.L., Amaratunge, H.C., Are, J.R., Ayele, M., Banks, T., Barbarita, J., Benton, J., Bimage, K., Blomha, D., Bontalia, J., Bonton, J., Bimage, K., Blomha, D., Bouck, J., Burch, P., Burket, C., Burrell, K.L., Byrd, N.C., Carron, T.F., Carter, M., Cavazos, S.R., Chacko, J., Chavez, D., Chen, R., Lu, R., Chen, R., Che
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tive 0; Mismatches 0;
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Matches 32; Conservative
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              DNA linear HTG 11-JUL-2002
*** SEQUENCING IN PROGRESS ***,
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Submitted (15-SEP-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA (Dass 1 to 111948)
Worley, K.C.
Direct Submission
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                                                                                                                                                                                              Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae;
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111948 bp
Rattus norvegicus clone CH230-4K5,
53 unordered pieces.
                                                                                                                                                                                            Chordata;
Rodentia;
                                                                                                AC094563.3 GI:21717879
HTG; HTGS_PHASE1.
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                                                                                                                                                                                              Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                  Norway rat.
Rattus norvegicus
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Project Information

RESULT 14 AC094563/c

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Mouse DNA sequence from clone RP23-198C2 on chromosome X, complete
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                                                                                                                                             NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
NOTE: This is a 'working draft' sequence. It currently consists of 53 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                     Chemistry: Dye-terminator Big bye: 100% of reads Assembly program: Phrap; version 0.90329 Consensus quality; 54807 bases at least Q40 Consensus quality; 64720 bases at least Q30
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Direct Submission

Submitted (23-MAY-2002) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshir. CB10 18A, UK. E-mail enquiries:

Cambridgeshir. CB10 18A, UK. E-mail enquiries:

humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk

On May 25, 2002 this sequence version replaced gi:21104114.

During sequence assembly data is compared from overlapping clones.

Where differences are found these are annotated as variations
together with a note of the overlapping clone name. Note that the
variation annotation may not be found in the sequence submission
corresponding to the overlapping clone, as we submit sequences with
only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all
regions were either double-stranded or sequenced with an alternate
chemistry or covered by high quality data (i.e., phred quality) -
30); an attempt was made to resolve all sequencing problems, such
as compressions and repeats; all regions were covered by at least
one plasmid subclone or more than one M13 subclone; and the
assembly was confirmed by restriction digest. The following
abbreviations are used to associate primary accession numbers given
in the feature table with their source databases: Em; EMBL; Sw;
swisspror; Tr:, TREMBL; Wp:, WORWEPP; Information on the WORWPEP
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Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia: Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    http://www.sanger.ac.uk/Projects/C_elegans/wormpep RP23-198C2 is
from the RPCI-23 Mouse PAC Library
constructed by the group of Pieter de Jong.
For further details see http://www.chori.org/bacpac/home.htm
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Best Local Similarity 100.0%; Pred. No. 0.00016;
Matches 32; Conservative 0; Mismatches 0;
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OM protein - protein search, using sw model

April 4, 2003, 14:26:00; Search time 45 Seconds (without alignments) 555.443 Million cell updates/sec Run on:

US-09-803-589-6 260

1 MAGSPLLWGPRAGGVGLLVL.....RVKRLETPAPQVPARRLLPP 260 OLIGO Gapop 60.0 , Gapext 60.0 Title: Perfect score: Sequence: Scoring table:

283224 seqs, 96134422 residues Searched:

Word size :

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

PIR\_73:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result

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No matches found

Search completed: April 4, 2003, 14:29:59 Job time : 46 secs

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GenCore version 5.1.4\_p5\_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

Run on:

April 4, 2003, 14:18:45; Search time 25 Seconds (without alignments) 431.354 Million cell updates/sec

US-09-803-589-6 260 1 MAGSPLLWGPRAGGVGLLVL......RVKRLETPAPQVPARRLLPP 260 Title: Perfect score: Sequence:

Scoring table:

OLIGO Gapop 60.0 , Gapext 60.0

112892 seqs, 41476328 residues Searched:

Word size :

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

SwissProt\_40:\* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description ü

No. Score Match Length DB Result

No matches found

Search completed: April 4, 2003, 14:27:08 Job time: 25 secs

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Perfect score:

Run on:

Sequence:

Scoring table:

Word size

Searched:

Database :

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61 RSVPRGEAAGAVQELARALAHLLEAERQERARAEAQEAEDQQARVLAQLLRVWGAPRNSD 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MAGSPLLWGPRAGGYGLLVLLIGIFRPPPALCARPVKEPRGLSAASPPLAETGAPRRFR 60
                                                                                                                 SEQUENCE FROM N.A.
Fricker L., McKinzle A.A., Sun J., Curran E., Qian Y., Yan L.,
Patterson S.D., Courchesne P.L., Richards B., Levin N., Mzhavia N.,
Devi L.A., Douglass J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-DEC_2001 (TrEMBLrel. 19, Created)
01-DEC_2001 (TrEMBLrel. 19, Last sequence update)
01-DEC_2001 (TrEMBLrel. 19, Last annotation update)
01-DEC_2001 (TrEMBLrel. 19, Last annotation update)
Similar to granilarlike neuroendocrine peptide.
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus.
                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
PROSAAS precursor (Granin-like neuroendocrine peptide precursor).
                                                                                                                                                                                     "Identification and characterization of proSAAS: a granin-like neuroendocrine peptide precursor that inhibits prohormone
                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match

100.0%; Score 260; DB 4; Length 260;
Best Local Similarity 100.0%; Pred. No. 2.9e-224;
Matches 260; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                   TISSUE-UTERUS;
Strausberg R.;
Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AF181562; AAF22643.1; -.
EMBL; BC002851; AAH02851.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Strausberg R.;
Submitted (AUG-2001) to the EMBL/GenBank/pDBJ databases.
EMBL; BC012263; AAH12263.1; -
SEQUENCE 258 AA: 27270 MM; 4197C8B077A20A22 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                              POTENTIAL. FF8E2722784B7A5C CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                   Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
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09esu4 mus musculu
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1674.133 Million cell updates/sec
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Copyright (c) 1993 - 2003 Compugen Ltd.
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                                                                                   OM protein - protein search, using sw model
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Q9QXU9
Q9QXV0
Q9ESU4
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sp_vertebrate:*
sp_unclassified:*
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sp_phage:*
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Maximum DB seq length: 200000000
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01-MAY-2000 (TrEMBLrel. 13,
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Match Length DB
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**Q9UHG2** 

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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
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MEDIINE-20098938; PubMed-10632593;
MEDIINE-20098938; PubMed-10632593;
Fricker L., McKinzle A.A., Sun J., Curran E., Qian Y., Yan L.,
Pattern S.D., Courchesne P.L., Richards B., Levin N., Mzhavia N.,
Devi L.A., Douglass J.;
"Identification and characterization of proSAAS, a granin-like
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mus musculus (Mouse).
Sukaryota: Metazoa: Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia: Eutheria: Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBI_TaxID=10090;
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                         63 VPRGEAAGAVQELARALAHLLEAERQERARAEAQEAEDQQARVLAQLLR 111
                                       63 VPRGEAAGAVQELARALAHLLEAERQERARAEAQEAEDQQARVLAQLLR 111
  Indels
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C84F688BDEB5313E CRC64;
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07452A460E868CF6 CRC64;
                                                                                                                                  01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
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  Mismatches
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EMBL, AFIBIS60; AAF2261.1; -.
MGD: MGI:135431; PCSKIn.
InterPro: IPR002965; P_rich_extensn.
PRINTS; PR01217; PRICHEXTENSN.
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processing.",
"Aurosci. 20:639-648(2000).
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260 AA; 27414 MW;
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EMBL; AF181561; AAF22642.1; -.
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258 AA; 27285 MW;
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 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                       ProSAAS precursor.
Rattus norvegicus (Rat).
                                                                                                              PRELIMINARY;
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PCSKIN OR SAAS.
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nes 49; Conser
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01-MAY-2000
49;
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MEDLINE-98292330; PubMed-9630436;
Donadel G., Marinos N., DeSilva M.G., Lu J., Notkins A.L., Lan M.S.;
"Molecular cloning and characterization of a highly basic protein, IA-4, expressed in pancreatic islets and brain.";
Neuroendocrinology 67:190-196(1998).
                                               Gaps
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Sciurognathi; Muridae; Murinae; Mus.
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    Length 258;
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                                             Indels
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Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
EMBL, AF293356; AAG09048.1;
SEQUENCE 187 AA: 19940 MW; 041F1888591A9B0 CRC64;
                                                                                                                                                                                                                                                                                   (TrEMBLrel. 16, Created)
(TrEMBLrel. 16, Last sequence update)
(TrEMBLrel. 16, Last annotation update)
    DB 11; L
2.8e-21;
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100.0%; Pred. No. 3e-14;
tive 0; Mismatches 0
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12.7%; Score 33; DB 100.0%; Pred. No. 2.8
                                                                                                              126 DDDPDAPAAQLARALLRARLDPAALAAQLVPAP 158
                                                                                     126 DDDPDAPAAQLARALLRARLDPAALAAQLVPAP 158
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Mammalia, Eutheria, Rodentia,
NCBI_TaxID=10090;
                                          33; Conservative
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                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                           Mus musculus (Mouse).
    Query Match
Best Local Similarity
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GenCore version 5.1.4\_p5\_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

Run on:

April 4, 2003, 14:26:46; Search time 28 Seconds (without alignments) 273.213 Million cell updates/sec

Title: Perfect score:

US-09-803-589-6 260

1 MAGSPLLWGPRAGGVGLLVL.....RVKRLETPAPQVPARRLLPP 260 Sequence:

OLIGO Gapop 60.0 , Gapext 60.0 Scoring table:

262574 seqs, 29422922 residues Searched:

Word size :

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database :

Issued\_Patents\_AA:\*

1: /cgn2\_6/ptodata/1/laa/5A\_COMB.pep:\*
2: /cgn2\_6/ptodata/1/laa/5B\_COMB.pep:\*
3: /cgn2\_6/ptodata/1/laa/6A\_COMB.pep:\*
5: /cgn2\_6/ptodata/1/laa/feB\_COMB.pep:\*
5: /cgn2\_6/ptodata/1/laa/FCTUS\_COMB.pep:\*
6: /cgn2\_6/ptodata/1/laa/FCTUS\_COMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

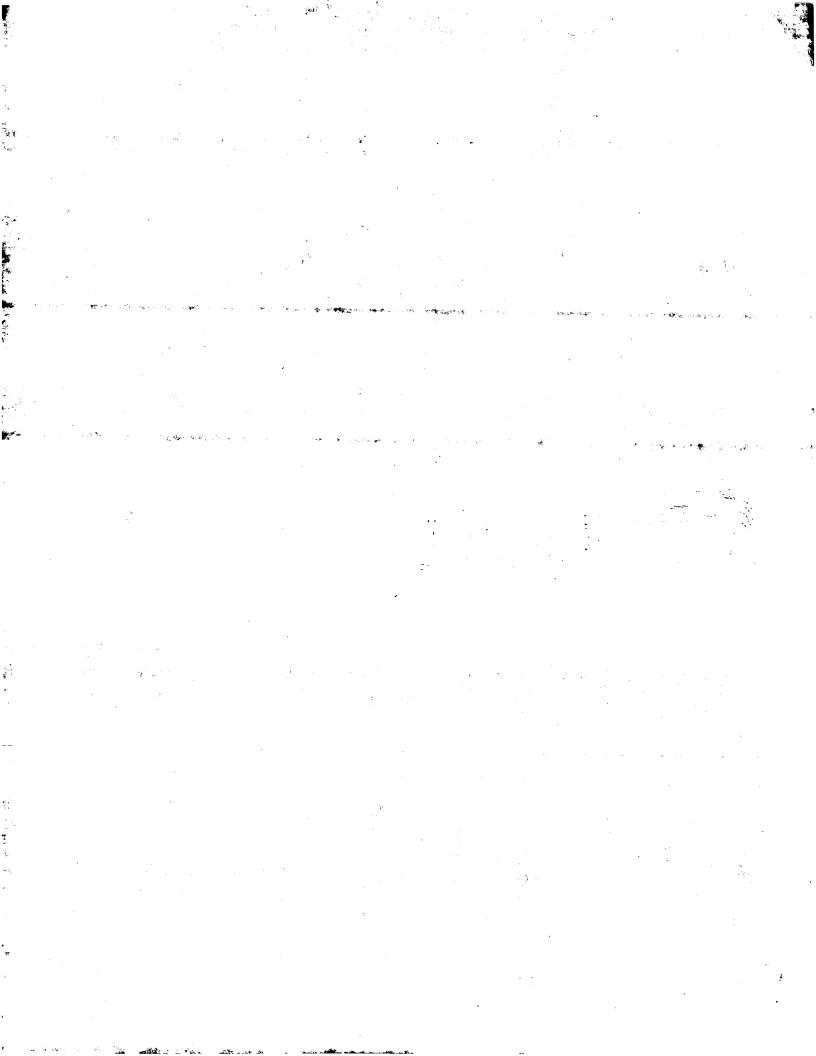
## SUMMARIES

Query Score Match Length DB Result

Description

No matches found

Search completed: April 4, 2003, 14:30:34 Job time: 28 secs



Perfect score:

Run on:

Sequence:

Scoring table:

Word size

Database

Searched:

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EEAGDETPDVDPELLRYLLGRILAGSADSEGVAAPRRLRRAADHDVGSELPPEGVLGALL 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; Score 260; DB 10;
; Pred. No. 1.4e-211;
0; Mismatches 0;
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Sequence 150; Application US/09984271

Sequence 150; Application US. US200040088A1

GENERAL INFORMATION:

APPLICANT: Rosen et al.

TITLE OF INVENTION:

FILE REFERENCE: PZ030P1
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CURRENT FILING DATE: 2001-10-29
PRIOR APPLICATION NUMBER: 09/482,273
PRIOR FILING DATE: 2000-01-13
PRIOR FILING DATE: 1999-07-14
PRIOR PELING DATE: 1999-07-14
PRIOR PILING DATE: 1998-07-15
PRIOR PELING DATE: 1998-07-15
PRIOR PELING DATE: 1998-07-15
PRIOR PELING DATE: 1998-07-15
PRIOR PELING DATE: 1998-07-15
                                                CURRENT FILICATION NUMBER: US 09/09/003, 2099
PRIOR APPLICATION NUMBER: US 09/128, 709
PRIOR PILING DATE: 1998-008-04
PRIOR PELICATION NUMBER: US 60/054, 645
PRIOR PELICATION NUMBER: US 60/054, 645
PRIOR PELICATION NUMBER: US 60/054, 910
PRIOR PELICATION NUMBER: US 60/054, 966
PRIOR PELICATION NUMBER: US 60/059, 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQ ID NOS: 14
SOFTWARE: FastSEQ for Windows Version 4.0
                                  us/09/803,589
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Best Local Similarity 100.0%;
Matches 260; Conservative 0;
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  FILE REFERENCE: 07334-325001
CURRENT APPLICATION NUMBER: CURRENT FILING DATE: 2001-0
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US-09-803-589-6
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PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 6, Appli
Sequence 150, App
Sequence 238, App
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Sequence 14, Appl
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993.461 Million cell updates/sec
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/cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
/cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
/cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
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GenCore version 5.1.4_p5_4578
Copyright (c) 1993 - 2003 Compugen Ltd.
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US-09-984-271-150
US-09-984-271-238
US-09-803-589-14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  248812 seqs, 61136040 residues
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Gapop 60.0 , Gapext 60.0
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Patent No. US20020112251A1
GENERAL INFORMATION:
APPLICANT: McCarthy, Sean A.
APPLICANT: Holtzman, Douglas A.
APPLICANT: Goodearl, Andrew D.J.
TITLE OF INVENTION: NOVEL GENES ENCOD
TITLE OF INVENTION: PROGNOSTIC, DIAG
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Maximum DB seq length: 200000000
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Match Length DB
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03-09-803-589-6

Score

Result

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0; Gaps

Length 260; Indels ö

Gaps ;

Length 175;

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18.8%; Score 49; DB 10; Length 17: 100.0%; Pred. No. 6.6e-34; ive 0; Mismatches 0; Indels
                                                  PRIOR FILING DATE: 1998-08-06
PRIOR APPLICATION NUMBER: US 60/054,966
PRIOR TILING DATE: 1997-08-06
PRIOR APPLICATION NUMBER: US 60/058,108
PRIOR FILING DATE: 1997-09-05
PRIOR FILING DATE: 1997-09-01
PRIOR FILING DATE: 1999-09-01
PRIOR APPLICATION NUMBER: US 09/388,279
PRIOR APPLICATION NUMBER: US 09/388,279
PRIOR APPLICATION NUMBER: US 09/388,279
NUMBER OF SEQ ID NOS: 14
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 14
FILING DATE: 1997-08-04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Search completed: April 4, 2003, 14:34:06
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Best Local Similarity 100.
Matches 49; Conservative
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CORGANISM: Mus musculus
US-09-803-589-14
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APPLICANT: HOLIZMAN, DOUGHES A.
APPLICANT: GOCGEAL, ANGTEW D.J.
APPLICANT: GOCGEAL, ANGTEW D.J.
APPLICANT: GOCGEAL, ANGTEW D.J.
APPLICANT: GOCGEAL, ANGTEW D.J.
APPLICANT: WOVEL GENES ENCODING PROTEINS HAVING
TITLE OF INVENTION: USES
FILE REFERENCE: 07334-32509
CURRENT APPLICATION NUMBER: US/09/803,589
PRIOR APPLICATION NUMBER: US 09/128,709
PRIOR APPLICANTION NUMBER: US 09/128,709
PRIOR FILING DATE: 1998-08-04
PRIOR APPLICANTION NUMBER: US 60/054,645
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                                                                                                                                                                                                                                            Query Match 19.6%; Score 51; DB 9; Length 149
Best Local Similarity 100.0%; Pred. No. 1.2e-35;
Matches 51; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Rosen et al.
TITLE OF INVENTION: 71 Human Secreted Proteins
FILE REFERENCE: PZ030P1
CURRENT FILING DATE: 2001-10-29
FRIOR APPLICATION NUMBER: 09/482,273
PRIOR APPLICATION NUMBER: 09/482,273
PRIOR APPLICATION NUMBER: 09/482,273
PRIOR APPLICATION NUMBER: 09/092,921
PRIOR APPLICATION NUMBER: 60/092,921
PRIOR FILING DATE: 1998-07-15
PRIOR FILING DATE: 1998-07-15
PRIOR APPLICATION NUMBER: 60/092,922
PRIOR FILING DATE: 1998-07-15
PRIOR APPLICATION NUMBER: 60/092,926
PRIOR FILING DATE: 1998-07-15
PRIOR APPLICATION NUMBER: 60/092,956
PRIOR FILING DATE: 1998-07-15
SOSTWARR: PATENTING DATE: 1998-07-15
SOSTWARR: PATENTING DATE: 1998-07-15
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; OTHER INFORMATION: Xaa equals stop translation
US-09-984-271-150
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Publication No. US20030040088A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             51; Conservative
                                                            TYPE: PRT
ORGANISM: Homo sapiens
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US-09-984-271-238
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Matches 51; Conserve
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US-09-803-589-14
         SEQ ID NO 150
LENGTH: 149
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Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
CDNA Library Preparation: Miklos I Brownstein (NHGRI), Shiraki
Toshiyuki and Piero Carninol (RIKEN)
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LiAMl1662 row: d column: 01
High quality sequence stop: 793.
High quality sequence stop: 793.
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B1546579
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602280321
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11H-MGC http://mgc.nci.nih.gov/.
National institutes of Health, Mammalian Gene Collection (MGC)
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BG703846
BG714685
BE383172
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BG703203
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BG716263
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AK002969
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BI603114
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Homo sapiens
744.3
744.0
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581.8
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BI546579
LOCUS
DEFINITION
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KEYWORDS
SOURCE
ORGANISM
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AUTHORS
TITLE
JOURNAL
COMMENT
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BI546579 603191602
BI603988 603244588
BI489332 603021593
BI602351 603251134
BI669134 603295564
BI458350 603198733
                                                April 12, 2003, 17:01:47; Search time 1577 Seconds (without alignments) 10054.142 Million cell updates/sec
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     GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                     16154066 seqs, 8097743376 residues
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Maximum Match 100%
Listing first 45 summaries
                                    nucleic search, using sw model
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length: 2000000000
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em_gss_hum:*
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75.5
75.2
75.1
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757 750.2 739.6 736.2 735.6

Score

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Minimum DB seq Maximum DB seq

Database

Title: Perfect score:

Sequence:

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Run on:

Scoring table:

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Pred. No. 1.1e-116;
5; Mismatches 25;
                /organism="Homo sapie
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                                                                                                                                                                                                                                                                                                                                                              77.3%;
96.0%;
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/clone="lba"NHI_MGC_96"
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/labh17
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Contact: Robert Strausberg, Ph.D.

Email: cgapbs-rémail.nih.gov
    Tissue Procurement: Miklos Palkovits, M.D., Ph.D.

CDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki
    Toshiyuki and Piero Carninci (RIKEN)
    CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
    DNA Sequencing by: Incyte Genomics, Inc.
    Clone distribution: MGC clone distribution information can be
    found through the I.M.A.G.E. Consortium/LLNL at:
    http://mage.llnl.gov
    Plate: LLAMI1725 row: o column: 22
    High quality sequence stop: 870.
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Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 878)
MIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
725 TGAGCTGCCCCTGAGGGCGTGCTGGGGGGGCGCTGCGTGTGAAACGCCTAGAGAACCC 784
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                                                                                               tch 76.6%; Score 750.2; DB 13 al Similarity 94.1%; Pred: No. 1.5e-115; 808; Conservative 5; Mismatches 38;
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B1603988.1 GI:15496928
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1. 951
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/lab_host="but108"
/note="Organ: brain; Vector: pcMV-SPORT6; Site_1: Not1:
Site_2: Ecory (destroyed); RNA source anonymous pool of 6 male brains, age range 23-27 yo. Library is ollygo-dT primed and directionally cloned (Ecory site is destroyed upon cloning). Average insert size 1.5 kb, insert size range 1-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 019. Note: this is a NIH_MGC Library."
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                                                                                                                                                                                                                                                                                      DB 13; Length 951;
                                                                                                                                                                                                                                                                                    75.5%; Score 739.6; DB 13; llarity 94.1%; Pred. No. 8.8e-114; Conservative 0; Mismatches 44;
 High quality sequence start: 25
High quality sequence stop: 824,
Location/Qualifiers
                                                                                                                                                                                                                                                                                                   Similarity
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BI489332.1 GI:15328560
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E I (basea 1 to 951)

S NIH-MGC http://mgc.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs rémail.nih.gov
Tissue Procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llni.gov
Plate: LLAM11480 row: j column: 24
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/lab_host="bHi0B"
/lab_host="DHi0B"
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National Institutes of Health, Mammalian Gene Collection (MGC)

L Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-rémail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.

CDNA Library Preparation: Miklos P. Brownstein (NHGRI), Shiraki
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:

thtp://mage.llnl.gov
Plate: LLAM1766 row: d column: 09

High quality sequence stop: 764.

Location/Qualifiers

I. .887
                                                                                                                                                                                                                                                                                                                                                                             BI602351 887 bp mRNA 11near EST 07-SEP-2001 603251134F1 NIH_MGC_96 Homo sapiens cDNA clone IMAGE:5302616 5',
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 887)
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Pred. No. 3.2e-113;
5; Mismatches 43; Indels 10;
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/db_xref="taxon:9606"
/clone="IMAGE:5302616"
/clone_lib="NIH_MGC_96"
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B1669134 764 bp mRNA linear EST 12-SEP-2001 603295564F1 NIH_MGC_96 Homo sapiens cDNA clone IMAGE:5314814 5', mRNA sequence.
B1669134 I GI:15583367
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Contact: Robert Strausberg, Ph.D.
Email: capbs-remail.nih.gov
Tissue Procurement: Milos Palkovits, M.D., Ph.D.
cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki
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                                TGAGGCGGCGGGGGCGGTGCAGGAGCTGCCGCGCGCGCTGCCGCATCTGCTGGTGGAGGCCGA
                                                                                                                                    251 rGAGGCGGCGGGGGGGGGGAGCTGGCGGGGGGGCGCTGGCGGCGATCTGCTGGAGGCCGA
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KEYWORDS
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AUTHORS
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BI458350
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286 c 294 g 108 t
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                                                                                                                                                                                                                                       /note-"Organ: brain; Vector: pBluescriptR (modified
                        Dona Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can found through the I.M.A.G.E. Consortium/LLNL at:
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
row: p column: 15
high quality sequence stop: 760.
Location/Qualifiers
I. 764
/organism="Homo sapiens"
//D.xref="Laxon:9666"
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
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                                                                                                                                                                                                                                                                                                                                                                                                                      Length 764;
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                                                                                                                                                                                                                                                                                                                                                                                                                     Score 735.6; DB 13;
Pred. No. 4.1e-113;
5; Mismatches 4;
                                                                                                                                                                       /clone="IMAGE:531484"
/clone_lib="NHH MGC_96"
/tissue_type="hypothalamus"
/lab_host="DHIOB"
                                                                                                                                                                                                                                                                                                                                                                                                                     75.1%;
98.7%;
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Contact: Robert Strausberg, Ph.D.

Email: cgapbs-rémail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
CDNA Library Preparation: Micheel J. Brownstein (NHGRI), Shiraki
Toshiyuki and Piero Carninci (RIKEN)
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM11702 row: b column: 10
High quality sequence stop: 838.
Location/Qualifiers
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleosto:
Mammalla; Eutherla; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 868)
NIH-MGC htt://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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                                                        CGCGGACTCCGAGGGGTGGCAGCCCCGCGCCGCCTCCGCCGTGCCGCCGACCACGATGT
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Pred. No. 4.8e-113;
5; Mismatches 38;
                                                                                                                                   735 GGCTCTGAGCTGCCCCTGAGGCCGTGCTGGGGGC 770
                                                                                                                                                     730 GGGCTCTGAGCTG-CCCCTGAGGGCGTGCTGGGGGC 764
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BI458350.1 GI:15249019
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94.3%;
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NIH_MGC_96 Homo sapiens cDNA clone IMAGE:5314354 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Issue Procurement: Miklos Palkovits, M.D., Ph.D.
cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki
Toshiyuki and Piero Carninci (RIKEN)
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           TITCGGCCGCCCCCCCGCGCTCTGCGCGCGCGCGATAAAGGAGCCCCGCGGGCCTAAGCGCA 180
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Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostos
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 908)
NIH MGC http://mgc.nci.nih.gov/.
NIH MGC http://mgc.nci.nih.gov/.
Unbublished (1999)
                                             CTGGCGCAGCTGCTGCGCGCTCTGGGGCGCCCCCGCAACTCTGATCCGGCTCTGGGCTTG
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                                                                                                                                    GACGACGCCCGACGCCTGCAGCGCAGCTCGCTCGCGCTCTGCTCCGCCCCCCTT
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GGATCCCGTGCACCCTGGGACCCAGAAGTGCC 881
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     603294847F1 NIH_MGC_96 NRNA sequence.
BI668879
BI668879.1 GI:15583112
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BI668879
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COMMENT

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/note="Organ: brain; Vector: pBluescriptk (modified pbluescript KS+); Site_1: Sall-xhol (gtcgap pbluescriptk KS+); Site_1: Sall-xhol (gtcgap pluescript KS+); Site_1: Sall-xhol (gtcgap pisce-selected for average insert size 2.3 kb and normalized to ROT 5. This is a primary library enriched for full-length clones and constructed using the cap-trapper method (Carninci, in preparation). Library constructed by M. Brownstein (NIMH/NHGRI, National Institutes of Health). Note: this is a NIH_MGC Library.
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Consortium (LLNL)
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Clone distribution: MGC clone distribution information
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
http://image.llnl.gov
Plate: LLAW11796 row: m column: 11
High quality sequence stop: 782.
Location/Qualifiers
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Pred. No. 9.4e-112;
5; Mismatches 36;
                                                                                                                                                  1. 908
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/lab_host="DH10B"
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BG709387 861 bp mRNA linear EST 07-MAY-2001 602673430F1 NIH_MGC_96 Homo sapiens CDNA clone IMAGE:4796286 5', mRNA sequence.
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
CDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki
Toshiyuki and Piero Carninci (RIKEN)
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
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                                                                                                                       ACGACGACCCCGACGCCTGCAGCGCAGCTCGCTCGCGCTCTGCTCCGCGCCCCTTG
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
CDNA Library Preparation: Miklohal J. Brownstein (NHGRI), Shiraki
Toshiyuki and Piero Carninci (RIKEN)
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://mage.llnl.gov
Plate: LLAM10672 row: I column: 07
High quality sequence stop: 745.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 745)
NIH-MGC http://mgc.nci.nih.gov/.
Mational Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                     856
                                                                                                 TG-AGCTGCCCCTGAGGGCGTGCTGGGGG--CGCTGCGTGCGTGTGAACGCCTAG-AGA 796
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                                                                                                                                722 TGAAGCTGCCCCCTGAGGCGTTGCTGGGGGGGCGCCTGCTGCTGTGAAACGCCTAGAAGA 781
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                                  CTCCGAGGGGGTGGCAGCCCCGCGCCGCCTCCGCCGTGCCGCCGACCACGATGTGGGGCTC
                                                    797 CCCCGGCGCCCCAGGTGCCTGCACCCTCTTGCCACCCTGAGCACTGCCCGGATCCC
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                                                                                                                                                                                                                                   GTGCACCCTGGGACCCAGAAGTGCCCCCCCCCCATCCCG 893
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Best Local Similarity 98.1
Matches 727; Conservative
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DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortlum/LLNL at:
http://image.llnl.gov
row: k column: 07
High quality sequence stop: 720.
Location/Qualifiers
                                                                                                                                                                                                                                                                               122 CGCGCTCTGCGCGCGGCGGTAAAGGAGCCCCGGCGCGCTAAGCGCAGCGTCTCCGCCCTT
                                                                                                                                                                                                                                                                                                                                                                                               GCCTGAGACTGGCGCTCCTCGCCGCTTCCGGCGGTCAGTGCCCCCGAGGTGAGGCGGCGGG
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8
                                                                                                                                                                                                                                    Length 861;
                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                   Score 721; DB 12;
Pred. No. 1.1e-110;
4; Mismatches 34;
                                                                                                                                                                                                                                   tch 73.6%; al Similarity 94.6%; 807; Conservative
                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                             Best Local
                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                        BASE COUNT
                                                                                                                                                                                                                                                                      27
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                                                      FEATURES
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/note="Organ: Drain; Vector: pBluescriptR (modified pBluescript KS+); Site_1: BamHI; Site_2: Sall-XhoI (gtcgap p. O. Myord T primed using primer 5'-rryryryryryryvN-3', size-selected for average insert size 2.3 kb and normalized to ROT 5. This is a primary library enriched for full-length clones and constructed using the constructed by M. Brownstein (NIMH/NHGRI, National Institutes of Health). Note: this is a NIH_MGC Library.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BI668984 11-SEP-2001 817 bp mRNA linear EST 12-SEP-2001 603294952F1 NIH_MGC_96 Homo sapiens cDNA clone IMAGE:5314213 5',
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 817)
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NIH-MGC http://mgc.ncl.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-rémail.nih.gov

Tissue Procurement: Mikhos Palkovits, M.D., Ph.D.

CDNA Library Preparation: Michael J. Brownstein (NHGRI), Shirston Library Preparation: Michael J. Brownstein (NHGRI), Shirston Library Arrayed by: The I.M.A.G.E. Consortium (LINL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be
                                                                                                                                                                                                                   860
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                                                                                                                                                      720 GCCCCCGTGACGAGCGTGCTGGGGCGCTGCTGCGTGTGAAACGCCTAGAGACCCCGGTC
                           GCCCCC - - TGAGGGCGTGCTGGGGGCGCTGTGCTGAAACGCCTAGAGACCCCGGG-C
                                                                                                                                                                                                              GCCCCAGGTGCCT-GCACGCCGCCTCTTGCCACCCTGAGC--ACTGCCCGGATCCCGTGC
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http://image.llnl.gov
Plate: LLAM1796 row: g column: 14
High quality sequence stop: 811.
Location/Qualifiers
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Pred. No. 2.5e-109;
5; Mismatches 12;
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/lab_host="DH10B"
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/clone_lib="NIH_MGC_96"
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96.9%;
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Matches 785; Conservative
                                                                                                                                                                                                                                                                                                                        ACCCTGGGACCCA 873
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BI668984
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Conservative
                                                                                                                                                                                                                                         Similarity
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ORIGIN
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bunmania; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 990)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rémail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
                 125
                                              185
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                                                                              245
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                               CCCCCCGCGCTCTGCGCGCGGCGGTAAAGAGGGCCCCGCGGCCTAAGCGCAAGCGTCTCCG
                                                             CCCTTGGCTGAGACTGGCGCTCCTCGCCGCTTCCGGCGGTCAGTGCCCCGAGGTGAGGCG
                                                                      186 CCCTTGGCTGAGACTGGCGCTCCTCGCCGCTTCCGGCGGCGGTGAGGCG
                                                                                                                           CTGCTGCGCGTCTGGGGGCGCCCCCCCCGCAACTCTGATCCGGCTCTGGGCTTTGGACGACGAC
                                                                                                                                                                                                                        GACGTGGACCCCGAGCTGTTGAGGTACTTGCTGGGACGGATTCTTGCGGGAAGCGC-GGA
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                                                                                                                                                                                                                                                                                                                                                                                 798 CCCGGCCCCCAGGTGCCTGCACGCCGCCT 827
                                                                                                                                                                                                                                                                                                                                                                                                                                                       mRNA sequence.
BF966686
BF966686.1 GI:12333901
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                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 11
BF966686/c
LOCUS
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KEYWORDS
SOURCE
ORGANISM
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                                                                                                                                                                                                                                                                                                                                                                   651
CDNA Library Preparation: Michael J. Brownstein (NHGRI), Sh
Toshhyuki and Piero Carninci (RIKEN)
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://mage.lnl.gov
Plate: LLAM10041 row: 1 column: 10
High quality sequence start: 9
High quality sequence start: 9
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                        Length 990;
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                                                                                                                                                                                                                                                                                                                        71.2%; Score 697; DB 12; 90.7%; Pred. No. 1.1e-106; Live 0; Mismatches 70;
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Query Match 71.2%; Score 696.6; DB 13
Best Local Similarity 97.7%; Pred. No. 1.2e-106;
Matches 722; Conservative 5; Mismatches 9;
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BM715636.1 GI:19028894
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KEYWORDS
SOURCE
ORGANISM
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BM715636
LOCUS
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1 (Dases 1 to 784)

2 NIH-MCC http://mgc.nci.nih.gov/.

National institutes of Health, Mammalian Gene Collection (MGC)

1 (Onbublished (1999)

2 Contact: Robert Strausberg, Ph.D.

2 Email: cgapbs-remail.nih.gov

3 Tissue Procurement: Miklos Palkovits, M.D., Ph.D.

3 Tissue Procurement: Miklos Palkovits, M.D., Ph.D.

4 Tissue Procurement: Miklos Palkovits, M.D., Ph.D.

5 CDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki

6 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

7 CORNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

8 CORNA Library Arrayed by: The I.M.A.G.E. Consortium/LLNL at:

8 CORNA Library Repeated by: The I.M.A.G.E. Consortium/LLNL at:

8 CORNA Library Repeated by: The I.M.A.G.E. Consortium/LLNL at:

8 CORNA Library Repeated by: The I.M.A.G.E. Column: 17

8 High quality sequence stop: 782.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BI668730 784 bp mRNA linear EST 12-SEP-2001 603293168F1 NIH_MGC_96 Homo sapiens cDNA clone IMAGE:5312320 5',
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="Organ: brain; Vector: pBluescriptR (modified pBluescript KS+); Site_1: BamHI; Site_2: Sall-XhoI (qtcg pBluescript KS+); Site_1: BamHI; Site_2: Sall-XhoI (qtcg plued user size 2: Sall-XhoI (qtcg size-selected for average insert size 2:3 kb and normalized to ROT 5. This is a primary library enriched for full:length clones and constructed using the cap-trapper method (carninci, in preparation). Library constructed by M. Brownstein (NIMH/NHGRI, National Institutes of Health). Note: this is a NIH_MGC Library."
                                 253
                                                                      771
                                                                                       252 CGCCGTGCCGCCGACCACCACGATGTGGGCTCTGAGCTGCCCCCTGAGGGCGTGCTGGGGGCG 193
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                                                                                                                                         CTGCTGCGTGTGAAACGCCTAGAGACCCCGGCGCCCCAGGTGCCTGCACGCCGCCTCTTG
                                                                                                                                                                                                               CCACCCTGAGCACTGCCCGGATCCCGTGCACCCTGGGACCCCAGAAGTGCCCCCGCCATCC
                                                                    CGCCGTGCCGCCGACCACGATGTGGGCTCTGAGCTGCCCCCTGAGGGCGTGCTGGGGGGCG
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/organism="Homo sapiens"
/db_xxef="taxon:9606"
/clone=Inb="NIH_MGC_96"
/tissue_type="hypothalamus"
/lab_host="DH108"
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BI668730
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Bonaldo, M.E., Lennon, G. and Soares, M.B.
Normalization and subtraction: two approaches to facilitate gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BM715636 707 bp mRNA linear EST 28-
UI-E-EJO-ahi-1-14-0-UI.r2 UI-E-EJO Homo sapiens CDNA clone
UI-E-EJO-ahi-1-14-0-UI 5', mRNA sequence.
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Length 784;
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746

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BI667137 771 bp mRNA linear EST 12-SEP-2001 603291530F1 NIH_MGC_96 Homo sapiens cDNA clone IMAGE:5310870 5',
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 771)
NIH-WG http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
COPA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki
Toshiyuki and Piero Carninci (RIKEN)
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone="IMAGE:5310870"
/clone_lib="NHH_MGC_96"
/tlssue_the"NHH_MGC_96"
/lab_host="BH108"
/note="Organ: brain; Vector: pBluescriptR (modified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
row: 1 column: 07
High quality sequence stop: 763.
                       CCAGGTGCCTGCACGCCGCCTCTTGCCACCCTGAGCACTGCCCGGATCCCGTGCACCCTG
                                                                                                                                                                                                                          GGGGGTGGCAGCCCCGCGCCGCCGCCGTGCCGCCGACCACGATGTGGGCTCTGAGCT
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/db_xref="taxon:9606"
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/dew_stage="fetal and adult"
/lab_host="DH10B (Life Technologies) (TI phage resistant)"
/note="Organ: eye; Vector: pT773-Pac (Pharmacia) with a modified pollylinker; Site_1: EcoR I; Site_2: Not I;
UT-E-E0 is a subtracted cDNA library constructed
according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806. 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT773-Pac vector: The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tags for this library are: fetal eyes, AGAATCAAGA; lens, CGATTAAGCA; eye anterior segment, AATGCCGAT; optic nerve, CCATTAAGTG; retina, CCGCG; Retina Foveal and Macular, GTCC; RPE and Chorold, ACCTA. This library was created for the program, Gene Discovery in the Visual System, supported by National Eye Institute (NEI):"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ä
                                                                                                 University of Iowa
451 Eckstein Medical Research Building Iowa City, IA 52242, USA
761: 319 315 8250
Fax: 319 315 9565
Email: msoares@blue.weeg.uiowa.edu
Tissue Procurement: Dr. Gregg Hageman
CDNA Library preparation: Dr. M. Bento Soares, Univeristy of Iowa
DNA Sequencing by: Dr. M. Bento Soares, Univeristy of Iowa
Clone Distribution: Researchers may obtain clones from Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /db_xref="taxon:9506"
/clone="UI-E-EJO-ahi-1-14-0-UI"
/clone="IIb="UI-E-EJO-ahi-1-14-0-UI"
/tissue_type="fetal eyes, lens, eye anterior segment, optic nerve, retina, Retina Foveal and Macular, RPE and Choroid"
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The following repetitive elements were found in this cDNA sequence: 256-326, >Gc_rich#Low_complexity
Seq primer: M13 Reverse
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                                                            Contact: Soares, MB
Program for Rat Gene Discovery and Mapping
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Pred. No. 7.9e-106;
0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Homo sapiens"
             Genome Res. 6 (9), 791-806 (1996)
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
constructed by M. Brownstein (NIMH/NHGRI, National
Institutes of Health). Note: this is a NIH_MGC Library.
                                                                                                             GTCTCCGCCCTTGGCTGAGACTGGCGCTCCTCGCCGCTTCCGGCGGCTCAGTGCCCCCGAGG 254
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                                                                             210 GTCTCCGCCCTTGGCTGAGACTGGCGCTCCTCGCCGCTTCCGGCGGTCAGTGCCCCGAGG
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                                                      3;
                                      DB 13; Length 771;
                                                      9; Indels
                                      Score 688.6; DB 13
Pred. No. 2.7e-105;
                                                      5; Mismatches
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                                      70.38;
97.78;
                                              Best_Local Similarity 97.7
Matches 724; Conservative
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                                      Query Match
               BASE COUNT
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/note="Organ: brain; Vector: pBluescriptR (modified pBluescript KS+); Site_1: BamHI; Site_2: SalI-XhoI (gtcgag p: Oligo-dT primed using primer 5'-TTTTTTTTTTTTTTTVN-3', size-selected for average insert size 2.5 kb and normalized to ROT 5. This is a primary library enriched for full-length clones and constructed using the cap-trapper method (Carninoi, in preparation). Library constructed by M. Brownstein (NIMH/NHGRI, National Institutes of Health). Note: this is a NIH_MGC Library.
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                                                                      Gene Collection (MGC)
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                                                                                    Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
CDNA Library Preparation: Michael J. Brownstein (NHGRI), Shi:
Toshiyuki and Piero Carninci (RIKEN)
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://inage.llnl.gov
Plate: LLAMIO703 row: o column: 21
High quality sequence stop: 763.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
I (bases 1 to 763)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (
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Pred. No. 5.7e-105;
5; Mismatches 19;
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/clone_lib="NIH_MGC_95"
/tissue_type="hippocampus"
/lab_host="DH10B"
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/organ1sm="Homo sapiens"
/db_xref="taxon:9606"
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Conservative
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46.1%; Pred. No. 1.5e-05;
tive 2; Mismatches 414;
US-09-078-166-2
US-09-997-467-2
US-09-993-593-593-3
US-09-288-292A-45
US-09-288-292A-45
US-09-484-970B-106
US-09-956-307B-11
US-08-956-307B-11
US-08-951-211-4
US-08-551-211-4
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US-09-404-650-3
5215881-2
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GENERAL INFORMATION:
APPLICANT: FLEISCHMAN, Robert D.
APPLICANT: WHITE, Owen R.
APPLICANT: WHITE, Owen R.
APPLICANT: WENGER, John C.
TITLE OF INVENTION: TUBERCULOSIS
FILE REFERENCE: 24366-20007,00
CURRENT APPLICATION NUMBER: US/09/103,840A
CURRENT FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 2
                                                                                                                                                                                                                                                                                                               ALIGNMENTS
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OTHER INFORMATION: "n" bases
OTHER INFORMATION: represent
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 Similarity
                                 SEQ ID NO 2
LENGTH: 4403765
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/cgn2_6/ptodata/1/ina/pcTUS_COMB.seq:*
               GenCore version 5.1.4_{-}p5_{-}4578 Copyright (c) 1993 - 2003 Compugen Ltd.
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US-08-845-998-7
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US-09-430-854-7
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US-08-690-473-1
US-08-859-821A-1
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US-08-843-659-1
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US-08-858-003-2
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Db 338356 TGCC--GCCGGCGCCGACACAGCCCGCCGTTCCGCCGGATCCGCCGGCCCGCGGTGCC 338413
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; OTHER INFORMATION: "n" bases at various positions throughout the sequence
; OTHER INFORMATION: represent a, t, c or g
US-09-103-840A-2
                                                                                                                                                                                                                                                                            Db 338116 CGCCTCCGATCCCACCGCCACCGCCGCCGCCGTCCGGGTCGATCCGCCGCCGCTGCCGCCGG 338175
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APPLICANT: WHITE, Owen R.
APPLICANT: WHITE, Owen R.
APPLICANT: FEASER, Olaste M.
APPLICANT: FEASER, Olaste M.
APPLICANT: FEASER, Olaste M.
TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM TITLE OF INVENTION: UNBERCUICASIS
FILE REFERENCE: 2486-24007.00
CURRENT APPLICATION NUMBER: US/09/103,840A
CURRENT FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PATENTIN VET: 2.1
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Pred. No. 0.00016;
0; Mismatches 434; Indels 9;
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Patent No. 6294328
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Similarity 44.9%;
51; Conservative 0
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APPLICANT: DUTRIC-ROSSET, Gilles
TITLE OF INVENTION: Streptogramins And Method For Preparing Same I
TITLE OF INVENTION: Mutasynthesis
FILE REFERENCE: Streptogramin genes
CURRENT APPLICATION NUMBER: US/08/765,907A
CURRENT FILING DATE: 1997-03-20
NUMBER OF SEO ID NOS: 17
SOFTWARE: Patentin Ver. 2.0
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APPLICANT: BLANC, Veronique
APPLICANT: THIBAUT, Denis
APPLICANT: BAMAS-JACQUES, Nathalie
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APPLICANT: COUZET, Joel
APPLICANT: BARRIERE, Jean-Claude
APPLICANT: DEBUSSCHE, Laurent
APPLICANT: FAMECHON, Alain
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APPLICANT: DUTRUC-ROSSET, Gilles
TITLE OF INVENTION: Streptogramins And Method For Preparing Same 1
TITLE OF INVENTION: Mutasynthesis
FILE REFERENCE: Streptogramin genes
                                                                           Length 888
                                                                                                    Indels
                                                                                                   3; Mismatches 327;
                                                                          Score 69.6; DB 4;
Pred. No. 0.00049;
                        ; TYPE: DNA
; ORGANISM: Streptomyces pristinaespiralis
US-08-765-907A-2
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APPLICANT: THIBATT, Denis
APPLICANT: BAMAS-JACQUES, Nathalie
APPLICANT: BLANCHE, Francis
APPLICANT: COUZET, Joel
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DEBUSSCHE, Laurent
FAMECHON, Alain
                                                                         7.18;
                                                                                      Best_Local Similarity 45.4
Matches 275; Conservative
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SEQ ID NO 2
LENGTH: 888
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FILLE REFERENCE: 2436-20007.00
CURRENT APPLICATION NUMBER: US/09/103,840A
CURRENT FILING DATE: 1998-06-24
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                                                                                                                                                                                                                                      Length 2888;
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                                                                                                                                                                                                                                    Score 69.6; DB 4;
Pred. No. 0.00047;
3; Mismatches 327;
CURRENT APPLICATION NUMBER: US/08/765,907A CURRENT FILING DATE: 1997-03-20 NUMBER OF SEQ ID NOS: 17 SOFTWARE: Patentin Ver. 2.0 SEQ ID NO 1
                                                                                                                  LENGTH: 2888
TYPE: DNA
ORGANISM: Streptomyces pristinaespiralis
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APPLICANT: FLEISCHMAN, ROBERT D. APPLICANT: WHITE, Owen R. APPLICANT: FRANSER, Claire M. APPLICANT: VENERK, John C.
                                                                                                                                                                                                                                    Query Match 7.1%;
Best Local Similarity 45.4%;
Matches 275; Conservative
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US-09-103-840A-1
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Query Match
Best Local Similarity 44.0
Matches 399; Conservative
                                                 APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                             LENGTH: 936 bases
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                                                                FILING DATE: 18 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                          TYPE: nucleic
STRANDEDNESS:
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Patent No. 568661
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: DNA Sequences Encoding Mutant Antiviral
TITLE OF INVENTION: Regulatory Proteins
NUMBER OF SEQUENCES:
ADDRESSEE: The Pennsylvania State University
STREET: 113 Technology Center
                                                                                                                                           Score 69.4; DB 4; Length 4
Pred. No. 0.00037;
0; Mismatches 291; Indels
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 720 Kb storage
COMPUTER: IBM PS/2
                                                                            ORGANISM: Mycobacterium tuberculosis
OTHER INFORMATION: H37Rv
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                                                                                                                                           n 7.1%;
Similarity 47.6%;
NUMBER OF SEQ ID NOS: 2
SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                             Best Local Similarity 47.6 Matches 267; Conservative
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CITY: University Park
STATE: PA
                                              LENGTH: 4411529
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US-09-103-840A-1
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                               SEQ ID NO 1
                                                                                                                                             Query Match
                                                                TYPE: DNA
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44.0%; Pred. No. 0.0071;
tive 4; Mismatches 488; Indels
                       6.0
OPERATING SYSTEM: MS-DOS 6.22
SOFTWARE: Microsoft Word for Windows
CURRENT APPLICATION DATA:
                                                                    US/08/018,977C
                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/726,071
FILING DATE: 05-JUL-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                          NAME: Thomas J. Monahan
REGISTRATION NUMBER: 29,835
REFERENCE/DOCKET NUMBER: 91-10
TELECOMMUNICATION INFORMATION:
TELEPAX: (814) 865-8277
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                   18-FEB-1993
IN: 435
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3935355 CCGCCGGCCGGCCGTTGCCGCCGACCCCGCCTTGGCCGCCGGCGAAGCCG 3935296
          3935706 CCGCCGTTGCCGCCGCTCACCCCTGGCTAGCCCGGTGCTGTTCAGGCCGCCT 3935647
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                                                                                                            611 ACGAGACACCCGACGTGGACCCCGAGCTGTTGAGGTACTTGCTGGGGACGGATTCTTGCGG 670
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Patent No. 6270989
GENERAL INFORMATION:
APPLICANT: Treco, Douglas A.
APPLICANT: Heartlein, Michael W.
APPLICANT: Heartlein, Michael W.
APPLICANT: Selden, Richard F
TITLE OF INVENTION: Protein Production and Delivery
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
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CLASSIFICATION: 435
PRIOR PAPLICATION DATE: US 08/243,391
APPLICATION NUMBER: US 08/243,391
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/789,188
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05-NOV-1991
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13-MAY-1994
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APPLICATION NUMBER: US
FILING DATE:
PRIOR APPLICATION DATE:
APPLICATION NUMBER: US
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MEDIUM TYPE: Floppy
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STATE: Massachus
COUNTRY: USA
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STREET: TWC
CITY: Lexi
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US-08-406-030A-3/c
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                                                                                                                                                                                                                                                                                                                 861 ACCCTGGGACCCAGAAGTGCCCCCGCCATCCCGCCACCAGGACTGCTCCCCGCCAGCACG 920
                                                                                                                                                                                                                                                                                                                                                                                                                                                      431 TGGACGACGACCCGACGCGCCTGCAGCGCAGCTCGCGCTCTGCTCCGCGCCCGGC 490
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: FRASER, CELAIRE M.
APPLICANT: VENTER, John C.
TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
TITLE OF INVENTION: TUBERCULÓSIS
FILE REFERENCE: 24366-20007.00
CURRENT APPLICATION NUMBER: US/09/103,840A
CURRENT APPLICATION NUMBER: 1998-06-24
NUMBER OF SEO ID NOS: 2
SOFTWARE: PATENTIN VET. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
681 CTCCGAGGGGTGGCAGCCCGCGCCCTCCGCCGTGCCGCCGACCATGTGGGCTC
                                                                                                                                     741 TGAGCTGCCCCCTGAGGGCGTGCTGGGGGCGCTGCGGTGTGAAACGCCTAGAGACCCC
                                                                                                                                                                                                                                                                          GGCGCCCCAGGTGCCTGCACGCCGCCTCTTGCCACCCTGAGCACTGCCCGGATCCCGTGC
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Pred. No. 0.011;
0; Mismatches 408; Indels 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; TYPE: DNA
. ORGANISM: Mycobacterium tuberculosis
; OTHER IPPORMATION: H37Rv
US-09-103-840A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1, Application US/09103840A
Patent No. 6294328
GENERAL INFORMATION:
APPLICANT: FLEISCHMAN, ROBERT D.
APPLICANT: WHITE, Owen R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 6.2%;
Best Local Similarity 46.4%;
Matches 365; Conservative
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LENGTH: 4411529
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2068 GGCGGGGCAGAAGGGCGCGGTGCCTGGGACCCGGGACCCGCGGGCAGCCCCGGGGGCGG 2009
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFWMARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                     APPLICANT: De Smet, Charles
APPLICANT: Lucas, Sophie
APPLICANT: Lucas, Sophie
APPLICANT: Lucas, Sophie
APPLICANT: Boon, Thierry
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
STREET: 600 Atlantic Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/08/845,998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY AGENT INFORMATION:
NAME: Van Amsterdam, John R.
REGISTRATION NUMBER: 40,212
REFERENCE/DOCKET NUMBER: L0461,
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)720-3500
TELEFAX: (617)720-3441
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                   Sequence 7, Application US/08845998
Patent No. 5879892
                                                                                                                                                                                                                                                                Van Baren, Nicolas
Coulie, Pierre G.
De Smet, Charles
Lucas, Sophie
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TYPE: nucleic acid
STRANDEDNESS: double
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                                                                                         2008 CACACGGCGC 1999
                                                826 CTCTTGCCAC 835
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FEATURE:
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                                                                                                                                                                                                                                                                APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY:
                                                                                                                                                                             US-08-845-998-7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            172 GAGCCCCCGCGCGCCTAAGCGCAGCGTCTCCCCCTTGGCTGAGACTGGCGCTCCTCGCCGC 231
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 59.6; DB 4; Length 4
Pred. No. 0.021;
1; Mismatches 391; Indels
                                                                                                                                                                  NAME: Grandhan, Patricia
REGISTRATION NUMBER: 32,227
REFERNENCE/DOCKET NUMBER: TKT95-01
TELEPHONE: (617) 861-6240
TELEPHONE: (617) 861-6240
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 4488 base pairs
FILING DATE: 05-NOV-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/11704
FILING DATE: 02-DEC-1993
                                                                                                          PCT/US92/09627
                                                                                                                                                                                                                                                                                                                                                                                                                              ; MOLECULE TYPE: DNA (genomic) US-08-406-030A-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity 45.3%;
                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/C
FILING DATE: 05-NOV-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches 331; Conservative
                                                                                                                                                                                                                                                                                                                                                                    TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                linear
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Best Local &
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                                                                                                                                                                                                755 AGGCGTGCTGGGGGCGCTGCTGCGTGTAAACGCCTAGAGACCCCGGGCGCCCCAGGTGC 814
461 AGCTCGCTCGCGCTCTGCTCCGCGCCCGCCTTGACCCTGCCGCCCTAGCAGCCCAGCTTG 520
                                                                       768 CACCTGTCGCACCCCGCGGCGGCGCCCATGAACATGCCGTCCGGGCTGCCGCACCC 827
                                                                                                             521 TCCCCGCGCCCGTCCCCGCGCGCGCTCCGACCCCGGCCCCCGGTCTACGACGACGGCC 580
                                                                                                                                          581 CCGC-GGGCCCGGATGCTGAGGAGGCAGGCGACGAGCACCCGACGTGGACCCCGAGCTG 639
                                                                                                                                                                                                                                                                                                         700 CCGCGCCGCCTCCGCCGTGCCGCCGACCACGATGTGGGCTCTGAGCTG-----CCCCCTG 754
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                                                                                                                                                                                                                                           640 TTGAGGTACTTGCTGGGACGGATTCTTGCGGGAAGCGCGGACTCCGAGGGGGGTGCCAGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRIY APPLICATION DATA:
APPLICATION NUMBER: US/09/206,537
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/845,998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 7, Application US/09206537 Patent No. 6130052 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Van Amsterdam, John R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Van Amsterdam, Joh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET: 600 A
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COUNTRY:
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948 ATCTGCGACTCGGACACGGACCCGCGCGCGAGCTCGAGGCGTTCGCGGAGCGCTTCAAGCAG 1007
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 59.4; DB 3; Length 4524;
Pred. No. 0.022;
0; Mismatches 401; Indels 12
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                           L0461/7008
             REFERENCE/DOCKET NUMBER: L046
TELECOMMUNICATION INFORMATION:
TELEPHONE: (611)720-3441
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 4524 base pairs
TYPE: nucleic acid
STRANDENESS: double
REGISTRATION NUMBER: 40,212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 6.1%;
Best Local Similarity 46.0%;
Matches 352; Conservative 0
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174..1433
                                                                                                                                                                                                                                                  MOLECULE TYPE: cDNA HYPOTHETICAL: NO ANTT-CENT
                                                                                                                                                                                                                                                                                                                                       ANTI-SENSE: NO FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY:
LOCATION:
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948 ATCTGCGGACTCGGACCCGCGCGGGGGCGCTTCGCGGGGGCGCTTCAAGCAG 1007
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     708 CCGGGCGCGCGCCTCCTGGGCGCTCCGCGCACCTCACCCGCATATGCACAGCCTGGGC 767
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                                                                                   461 AGCTCGCTCGCGCTCTGCTCCGCGCCCTTGACCCTGCCGCCCTAGCAGCCCAGCTTG
                                                                                                                                                           521 TCCCCGCGCCCCTCCCCGCGCGCGCTCCGACCCCGGCCCCCGGTCTACGACGACGGCC
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; Patent No. 5876923
; GENERAL INCRATION:
APPLICANT: Leopardi, Rosario
APPLICANT: Rolzman, Bernard
; TITLE OF INVENTION: HERPES SIMPLEX VIRUS ICP4 AS AN
; TITLE OF INVENTION: INHIBITOR OF APOPTOSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/690,473
FILING DATE: 26-JUL-1996
CLASSIFICATION: 435
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NAME: Highlander, Steven L.
REGISTRATION NUMBER: 37,642
REFERENCE/DOCKET NUMBER: ARCD:239
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512/418-3000
TELEPHONE: 512/474-7577
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Arnold, White & Durkee STREET: P.O. Box 4433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBB PC COMPATIBLE
OPPERATING SYSTEM: PC-DOS/MS-DOS
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INFORMATION FOR SEQ ID NO:
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CORRESPONDENCE ADDRESS:
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US-08-690-473-1
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1248 AAGCGGACTTCCATCGC-CGCGCCCGAGAAGCGCTCCCTCGAGGC 1291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                 APPLICANT: Van Baren, Nicolas
APPLICANT: Coulie, Pierre G.
APPLICANT: Coulie, Charles
APPLICANT: De Smet, Charles
APPLICANT: Boon, Thierry
TITLE OF INVENTION: LEUKEMIA ASSOCIATED GENES
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Wolf, Greenfield & Sacks, P.C. STREET: 600 Atlantic Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Van Amsterdam, John R.
REGISTRATION NUMBER: 40,212
REFERNCE/DOCKET NUMBER: L0461/7008
TELECOMMINICATION: TELEPHONE: (617)720-3500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/09/430,854
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/845,998
                                                                                                                           Sequence 7, Application US/09430854 Patent No. 6271019
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: (617)720-2441
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
LENGTH: 4524 base pairs
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STRANDEDNESS: double
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US-09-430-854-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: CDNA HYPOTHETICAL: NO
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Best Local Similarity
Matches 352; Conserv
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                                                                                                                           CIGGGGCAGCAIGGCGGGGTCGCCGCTGCTGGGGGCCGCGGGGCCGGGGGCGTCGGCCT 107
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                                                                                                      13;
                                                                                Length 4257;
                                                                            Score 59.2; DB 2; Length 4
Pred. No. 0.024;
0; Mismatches 453; Indels
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                                                                            Similarity 44.5%;
4; Conservative
      LENGTH: 4257 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE CHARACTERISTICS
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US-09-259-821A-1
                                                                                                    374;
                                                      US-08-690-473-1
                                                                            Query Match
Best Local 9
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Matches
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APPLICANT: ROIZWAN, BERNARD
TITLE OF INVENTON: HERPES SIMPLEX VIRUS ICP4 IS AN INHIBITOR OF
PILE REFERENCE: ARCD:317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 4257
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Best Local Similarity 44.5%; Pred. No. 0.024;
Matches 374; Conservative 0; Mismatches 453;
                                                                                                                                                         FILE REFERENCE: ARCD: 317
CURRENT APPLICATION NUMBER: US/09/259, 821A
CURRENT FILING DATE: 1999-03-01
PRIOR APPLICATION NUMBER: 08/690,473
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PatentIn Ver. 2.1
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408 CAACTCTGATCCGGCTCTGGGCTTGGACGACGCCCCGACGCGCCTGCAGCGCAGCTCGC 467
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/458,568A
FILING DATE: 02-JUNE-1995
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APPLICATION NUMBER: US 08/065,146
FILING DATE: 05-MAY-1993
CLASSIFICATION: 435
ATTORNEY/ABENT INFORMATION:
RAME: Leary Ph.D., Kathryn R.
REGISTRATION NUMBER: 36,317
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TELECOMMUNICATION INFORMATION
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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US-08-458-568A-11/c
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3074 CCCTGGGGCCTGGGGCCGCTGGATGCGGCTGGATGCGCCGAGATCCCGGACC 3133
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Pred. No. 0.024;
0; Mismatches 453; Indels 13; Gaps
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                                                                                                                                                                                   Sequence 1, Application US/08843659
Patent No. 6218103
GENERAL INFORMATION:
APPLICANT: Leopardi, Roasrio
APPLICANT: Roizman, Bernard
TITLE OF INVENTION: HERPES SIMPLEX VIRUS US3 AND ICP4 AS
TITLE OF INVENTION: INHIBITORS OF APOPTOSIS
NUMBER OF SEQUENCES: 6
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
ODERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/843,659
FILING DATE: CONCURRENTLY Herewith
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ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
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NAME: Highlander, Steven L.
REGISTRATION NUMBER: 37,642
REFERENC/DOCKET NUMBER: ARSB:519
TELECOMMUNICATION INFORMATION:
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TELERAX: (512) 474-7577
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 4257 base pairs
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Best Local Similarity 44.5%
Matches 374; Conservative
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CLASSIFICATION: 435
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                                                                                                                                                           US-08-843-659-1
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Sequence 11. Application US/08458568A
Patent No. 5821339
GENERAL INFORMATION:
APPLICANT: Schaffer, Priscilla A.
APPLICANT: Yeh, Lily
TITLE OF INVENTION: Compositions and Methods for Treatment of Herpesvirus
TITLE OF INVENTION: Infections
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSES: Woodcock, Washburn, Rurtz, Mackiewicz & No. 5821339ris
STREET: One Liberty Place, 46th floor
CITY: Philadelphia
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2663 GECCCCCTCCACGCCCCGG--GGCCCGAGCCCGCCCCGCCCAGCCCGGGGGCCCCG
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                                                                                                                                                                 TCGCGCTCTGCTCCGCGCCCGCCTTGACCCTGCCGCCCTAGCAGCCCAGCTTGTCCCCGC
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: TELEFAX: (215) 568-3100
: INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 12001 h--
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time : 9767 secs

Job

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                                                                                                                                                                         Score 59.2; DB 1; Length 12001;
Pred. No. 0.023;
0; Mismatches 453; Indels 13;
                                                                                         ORIGINAL SOURCE:
CRGANISM: Herpes simplex virus
STRAIN: Herpes Simplex Virus Type 1
US-08-458-568A-11
                            TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
                                                                                                                                                                       6.0%;
Best Local Similarity 44.5%;
Matches 374; Conservative (
TYPE: nucleic acid
STRANDEDNESS: double
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Search completed: April 12, 2003, 21:16:56

Appli Appli

Sequence

Sequence 47, Sequence 8, A

Sequence 1, Ap Sequence 20, A Sequence 45, A

Sequence 45, Appl Sequence 15, Appl Sequence 1, Appli Sequence 7852, Appl Sequence 292, Appl Sequence 293, Appl Sequence 529, Appl Sequence 48, Appl Sequence 48, Appl Sequence 48, Appl Sequence 18, Appl Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 116, Appli Sequence 116, Appli Sequence 17855, Appli

Sequence Sequence

Sequence:

Run on:

Searched:

Database

. 9 Result

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APPLICANT: MCCATLLY, Sean A.
APPLICANT: Holtzman, Douglas A.
APPLICANT: Holtzman, Douglas A.
APPLICANT: Goodearl, Andrew D.J.
TITLE OF INVENTION: NOVEL GENES ENCODING PROTEINS HAVING
TITLE OF INVENTION: NOVEL GENES ENCODING PROTEINS HAVING
TITLE OF INVENTION: USES
TITLE OF INVENTION: USES
CURRENT APPLICATION NUMBER: US/09/803,589
CURRENT APPLICATION NUMBER: US 09/128,709
PRIOR APPLICATION NUMBER: US 60/054,645
PRIOR PLILNG DATE: 1998-08-04
PRIOR FILING DATE: 1997-08-04
PRIOR PLILNG DATE: 1997-08-06
PRIOR PLILNG DATE: 1997-08-06
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PRIOR PLILNG DATE: 1997-09-05
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PRIOR FILING DATE: 1997-09-05
PRIOR FILING DATE: 1999-09-01
PRIOR PLILNG DATE: 1999-09-01
PRIOR PLILNG DATE: 1999-09-01
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0 US-10-013-388-2
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0 US-09-976-740-45
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10 US-09-912-228-1
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10 US-09-976-740-48
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US-09-772-656-5
US-09-772-656-9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 5, Application US/09803589 Patent No. US20020112251A1 GENERAL INFORMATION:
NUMBER OF SEQ ID NOS: 14
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Sequence 1701, Ap
Sequence 71, Appl
                                                                                                                                                               April 12, 2003, 18:14:02 ; Search time 151 Seconds (without alignments) 5687.068 Million cell updates/seb
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1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
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14: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*
                      GenCore version 5.1.4_p5_4578
Copyright (c) 1993 - 2003 Compugen Ltd.
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0 US-09-80-107-1701
0 US-09-960-352-71
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 1.0
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Sequence 58, Application US/09984271

-09-984-271-58

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GENERAL INFORMATION:
APPLICANT: ROSen et al.
TITLE OF INVENTION: 71 Human Secreted Proteins
FILE REPERENCE: P2030P1
CURRENT APPLICATION NUMBER: US/09/984,271
CURRENT APPLICATION NUMBER: 09/482,273
PRIOR APPLICATION NUMBER: 09/482,273
PRIOR FILING DATE: 2000-01-13
PRIOR PILING DATE: 1999-07-14
PRIOR APPLICATION NUMBER: 60/092,921
PRIOR PILING DATE: 1998-07-15
PRIOR APPLICATION NUMBER: 60/092,922
PRIOR APPLICATION NUMBER: 60/092,926
PRIOR APPLICATION NUMBER: 60/092,956
PRIOR APPLICATION NUMBER: 60/092,956 93.2%; Query Match 93.2 Best Local Similarity 98.9 Matches 955; Conservative ; TYPE: DNA ; ORGANISM: Homo sapiens US-09-984-271-58 314 14 71 74 134 131 194 191 254 250 308 374 367 434 427 487 554 547 614 607 464 à g

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                                                                                                                  195 GTCTCCGCCCTTGGCTGAGACTGGCGCTCCTCGCCGCTTCCGGCGGCGGTCAGTGCCCCGAGG
                                                                                                                                     255 TGAGCCGCGGGGGGGGGGGAGCTGGCGCGGGCGCTGGCGCATCTGCTGGAGGCCGA
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                                                    375 GGCGCAGCTGCTGCGCGTCTGGGGCGCCCCCCGCAACTCTGATCCGGCTTGGGATTGGA
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APPLICANT: Scherf, Uwe
APPLICANT: Scherf, Uwe
APPLICANT: Gene Logic, Inc.
TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer
FILE REPERENCE: 44921-5028-WO
CURRENT APPLICATION NUMBER: US/09/880,107
CURRENT FILING DATE: 2001-06-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          915 AGCACGTCCAGAGCAACTTACCCCGGCCAGC 945
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Patent No. US20020142981A1
PAPERAL INFORMATION:
APPLICANT: Horne, Darci T.
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US-09-880-107-1701/c
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APPLICANT: HOLTZMAILON: Douglas A.
APPLICANT: HOLTZMAILON: Douglas A.
APPLICANT: HOLTZMAILON: Douglas A.
TAPLICANT: GOOGGALI, ANGLEW D.J.
TITLE OF INVENTION: NOVEL GENES ENCODING PROTEINS HAVING
TITLE OF INVENTION: USES
TITLE OF INVENTION: USES
TITLE OF INVENTION: USES
CURRENT APPLICATION NUMBER: US/09/803,589
CURRENT FILING DATE: 1998-09-04
PRIOR APPLICATION NUMBER: US 60/054,645
PRIOR APPLICATION NUMBER: US 60/054,645
PRIOR FILING DATE: 1997-08-04
PRIOR FILING DATE: 1997-08-06
PRIOR FILING DATE: 1997-08-06
PRIOR FILING DATE: 1997-08-06
PRIOR FILING DATE: 1997-09-05
PRIOR FILING DATE: 1997-09-05
PRIOR FILING DATE: 1999-09-01
SPRIOR FILING DATE: 1999-09-01
PRIOR FILING DATE: 1999-09-01
PRIOR FILING DATE: 1999-09-01
SPRIOR FILING DATE: 1999-09-01
PRIOR FILING DATE: 1999-09-01
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                                                                                                                                                 CCCGTGCACCCTGGGACCCAGAAGTGCCCCCGCCATCCCGCCACCAGGACTGCTCCCCGC
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Pred. No. 1.5e-104;
5; Mismatches 157; Indels
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Best Local Similarity 75.1%;
Matches 699; Conservative
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Patent No. US20020112251A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; NAME/KEY: CDS
; LOCATION: (106)...(630)
US-09-803-589-13
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ORGANISM: Mus musculus
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Sequence 2663, Application US/09983965

Patent No. US20020137160A1

GENERAL INFORMATION:

APPLICANT: Warren, Wesley C.

APPLICANT: Tao, Nengbing

APPLICANT: Byatt, John C.

TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION

TITLE OF INVENTION: NUMBER: US/09/983,965

CURRENT APPLICATION NUMBER: US 09/465,231

PRIOR PILING DATE: 1999-12-15

PRIOR APPLICATION WORBER: US 00/113,678

PRIOR FILING DATE: 1998-12-17

NUMBER OF SEQ ID NOS: 5912
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 CCCGACGCGCCGACGCGCAGCTCGCCGCGCCCTGCTCCGCACCCGCCTGGACCCGGGC 120
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                                                                              453 TGCAGCGCAGCTCGCTCGCGCTCTGCTCCGCGCCCTTGACCCTGCCGCCCTAGCAGC
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         CTGGGGCGCCCCCCCCAACTCTGATCCGGCTCTGGGCTTGGACGACGACCCCGACGCGCC
                                          122 CTGGGGGGGCACCCGCACCAGTGACCCAGCCTGGGCCTGGAGAACGACCCCGACGCGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; OTHER INFORMATION: Clone ID: 10-LIB3058-043-Q1-K1-C5 US-09-983-965-2663
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ORGANISM: Bos taurus
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LENGTH: 372
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APPLICANT: Tao, Mengbing
APPLICANT: Tao, Mengbing
APPLICANT: Tao, Mengbing
APPLICANT: Byatt, John C.
APPLICANT: Mathialagan, Nagappan
TITLE OF INVENTION: WIGCLE AND FAT DEPOSITION
FILE REFERENCE: 16511.006/37-21(10298)C
CURRENT APPLICATION NUMBER: US/09/960,352
CURRENT FILING DATE: 2001-09-24
NUMBER OF SEQ ID NOS: 15112
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                                                                                                                                                                                              . OTHER INFORMATION: Genbank Accession No. US20020142981A1 D59847
US-09-880-107-1701
                                                                                                                                                                                                                                                                   10; Length 301;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 274.4; DB 10; Length 349;
Pred. No. 1.2e-52;
0; Mismatches 46; Indels 0;
                                                                                                                                                                                                                                                                                                     0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA
ORGANISM: Bos taurus
OTHER INFORMATION: Clone ID: 01-LIB3057-002-Q1-K1-A9
                                                                                                                                                                                                                                                                 Score 276.6; DB 1
Pred. No. 3.8e-53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      943 AGCCAGCCCTCTCACCCGAGGATCCCTACCCCTGGC 979
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1; Mismatches
PRIOR APPLICATION NUMBER: US 60/211,379
PRIOR FILING DATE: 2000-06-14
PRIOR APPLICATION NUMBER: US 60/237,054
PRIOR FILING DATE: 2000-10-02
NUMBER OF SEQ ID NOS: 3950
SOFTWARE: PATENTIN VEY. 2.1
SEQ ID NO 1701
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 71, Application US/09960352
Patent No. US20020137139A1
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86.8%;
                                                                                                                                                                                                                                                               Query Match 28.3%;
Best Local Similarity 99.6%;
Matches 276; Conservative
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                                                                                                                                                                   ORGANISM: Homo sapiens
FEATURE:
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US-09-960-352-71
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Matches 302;
                                                                                                                                                       TYPE: DNA
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                                                                                                                                    LENGTH:
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261 GGCGGGGGCGGTGCAGGAGCTGGCGCGGGGGCGCATCTGCTGGAGGCCGAACGTCA 320
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APPLICANT: Lees, Robert S.
APPLICANT: Lees, Sohert S.
APPLICANT: Law, Simon W.
APPLICANT: Arjona, Anibal A.
TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING
TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -----GGGCAGCTGCTGCGCGTCTGGGGCGCCCCCGCAACTCTGATCCGGCTCTGGGC
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                                                                                                                                                                                                                                                                                                                                      Length 1614;
                                                                                                                                                                                                                                                                                                                                                       Pred. No. 1.4e-08;
0; Mismatches 278;
PRIOR APPLICATION NUMBER: US 08/979,608
PRIOR FILING DATE: 1997-11-26
PRIOR APPLICATION NUMBER: US 60/031,930
PRIOR PELING DATE: 1996-11-27
PRIOR FILING DATE: 1997-06-03
NUMBER OF SEQ ID NOS: 53
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 45
LENGTH: 1614
                                                                                                                                                                                                                                                                                                                                      Score 75.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           676 CCGCCGCCGCAGCCACAGCCGCC 701
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                                                                                                                                                                                                                                                                                                                                  Query Match 7.7%;
Best Local Similarity 48.6%;
Matches 275; Conservative
                                                                                                                                                                                                                                                                      ; LOCATION: (1)...(1614)
US-09-976-740-45
                                                                                                                                                                                               TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                        NAME/KEY: CDS
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                                                                                                          Sequence 3684, Application US/09983965

Patent No. US20020137160a1

GENERAL INFORMATION:

APPLICANT: Warren, Wesley C.

APPLICANT: Byart, John C.

TITLE OF INVENTION: NUCLEIC ACLD AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND FILE REFERENCE: 37-21(10297)C

CURRENT FILING DATE: 2001-10-26

PRIOR PAPLICATION NUMBER: US/09/983,965

CURRENT FILING DATE: 1999-12-15

PRIOR FILING DATE: 1999-12-15

PRIOR FILING DATE: 1999-12-17

SEQ ID NOS: 5912

LENOTH: 342
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Lees, Robert S.
APPLICANT: Law, Simon W.
APPLICANT: Law, Simon W.
APPLICANT: Arjona, Anibal A.
ITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING
TITLE OF INVENTION: ATHEROSCLEROSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 17.1%; Score 167; DB 10; Length 3. Best Local Similarity 81.7%; Pred. No. 7.9e-29; Matches 205; Conservative 0; Mismatches 45; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; OTHER INFORMATION: Clone ID: 43-LIB3058-043-Q1-K1-C12 US-09-983-965-3684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILE REFERENCE: 10797-004001
CURRENT APPLICATION NUMBER: US/09/976,740
CURRENT FILING DATE: 2001.10-12
PRIOR APPLICATION NUMBER: 09/616,289
PRIOR FILING DATE: 2000-07-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 45, Application US/09976740; Sequence 45, Application US/09976740; Publication No. US20020194633A1; GENERAL INFORMATION:
  361 GAACTACCCCT 372
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ORGANISM: Bos taurus
                                                                                                -09-983-965-3684
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GEMERAL INFURMATION:
APPLICANT: Lees, Ann M.
APPLICANT: Lees, Robert S.
APPLICANT: Lees, Robert S.
APPLICANT: Lees, Robert S.
APPLICANT: Lees, Robert S.
APPLICANT: Lew Simon W.
APPLICANT: Arjona, Anibal A.
APPLICANT: Arjona, Anibal A.
APPLICANT: Arjona, Anibal A.
TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING
TITLE OF INVENTION: ATHEROSCLEROSIS
TITLE OF INVENTION: ATHEROSCLEROSIS
TITLE OF INVENTION: ATHEROSCLEROSIS
CURRENT FILING DATE: 2001-12-17
PRIOR APPLICATION NUMBER: US 09/517,849
PRIOR FILING DATE: 2000-07-14
PRIOR APPLICATION NUMBER: US 08/979,608
PRIOR FILING DATE: 1997-11-27
PRIOR APPLICATION NUMBER: US 60/031,930
PRIOR APPLICATION NUMBER: US 60/031,930
PRIOR APPLICATION NUMBER: US 60/048,547
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48.6%; Pred. No. 1.4e-08;
tive 0; Mismatches 278;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 48.6
Matches 275; Conservative
                        US20020152485A1
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; LOCATION: (1)...(1614)
US-10-023-523-45
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FILE REFERENCE: 10797-004001
CURRENT APPLICATION UNDBER: US/10/023,529
CURRENT APPLICATION UNDBER: US/10/023,529
CURRENT FILING DATE: 2001-12-17
PRIOR APPLICATION NUMBER: 09/616,289
PRIOR FILING DATE: 2000-07-14
PRIOR FILING DATE: 2000-03-02
PRIOR FILING DATE: 2000-03-02
PRIOR FILING DATE: 1997-11-26
PRIOR PELLOR DATE: 1997-11-26
PRIOR FILING DATE: 1996-11-27
PRIOR FILING DATE: 1997-06-03
NUMBER OF SEQ ID NOS: 53
NUMBER OF SEQ ID NOS: 53
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US-10-023-523-45
; Sequence 45, Application US/10023523
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ORGANISM: Homo sapiens
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; LOCATION: (1)...(1614)
US-10-023-529-45
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APPLICANT: Lees, Ann M.
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APPLICANT: Lees, Robert S.
APPLICANT: Lees, Robert S.
APPLICANT: Lew, Sindon W.
APPLICANT: Law, Sindon W.
TITLE OF INVENTION: ANIbal A.
TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING
TITLE OF INVENTION: ATHEROSCLEROSIS
FILE REFERENCE: 10797-004001
CURRENT APPLICATION NUMBER: US/10/023,529
CURRENT FILING DATE: 2001-12-17
PRIOR APPLICATION NUMBER: US 09/517,849
PRIOR APPLICATION NUMBER: US 09/517,849
PRIOR PRILING DATE: 2000-03-02
PRIOR APPLICATION NUMBER: US 60/919,608
PRIOR FILING DATE: 1997-11-26
PRIOR FILING DATE: 1997-11-26
PRIOR FILING DATE: 1997-11-27
PRIOR APPLICATION NUMBER: US 60/048,547
PRIOR APPLICATION NUMBER: US 60/048,547
PRIOR FILING DATE: 1997-06-03
NUMBER OF SEQ ID NOS: 53
SOFTWARE: FESTSED for Windows Version 4.0
           2969 GGCGGGCGGACCTGGAGCGCATCTGCCGGATGGTGCGGCGGCGGCAGCAGCG 3028
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Matches 275; Conservative
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US-10-023-529-50
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APPLICANT: Law, Simon W.
APPLICANT: Law, Simon W.
TITLE OF INVENTION: NOVELLOW DENSITY LIPOPROTEIN BINDING
TITLE OF INVENTION: NOVELLOW DENSITY LIPOPROTEIN BINDING
TITLE OF INVENTION: ATHEROSCLEROSIS
FILE REFERENCE: 10797-004001
CURRENT APPLICATION NUMBER: US/09/976,740
PRIOR PILING DATE: 2001-10-12
PRIOR APPLICATION NUMBER: US 08/979,608
PRIOR APPLICATION NUMBER: US 08/979,608
PRIOR APPLICATION NUMBER: US 60/031,930
PRIOR PILING DATE: 1997-11-26
PRIOR FILING DATE: 1996-11-27
PRIOR FILING DATE: 1996-11-37
PRIOR FILING DATE: 1996-11-37
PRIOR FILING DATE: 1996-11-37
PRIOR FILING DATE: 1997-06-03
NUMBER OF SEQ ID NOS: 53
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RESULT 11
US-09-976-740-50
; Sequence 50, Application US/09976740
; Publication No. US20020194633A1
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Law, Simon W.
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US-09-976-740-50
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LENGTH: 12425
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TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING
TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING
TITLE OF INVENTION: ATHEROSCLEROSIS
TITLE OF INVENTION: ATHEROSCLEROSIS
FILE REFERENCE: 10797-004001
CURRENT APPLICATION NUMBER: US/09/616,289
PRIOR APPLICATION NUMBER: US/09/616,289
PRIOR APPLICATION NUMBER: US/09/616,289
PRIOR PILING DATE: 2000-03-02
PRIOR FILING DATE: 2000-03-12
PRIOR FILING DATE: 1900-11-27
PRIOR APPLICATION NUMBER: US 60/031,930
PRIOR PILING DATE: 1990-11-27
PRIOR PILING DATE: 1990-11-27
PRIOR PAPLICATION NUMBER: US 60/048,547
PRIOR PELING DATE: 1990-11-27
                                                                                       730 GATGTGGGCTCTGAGCTGCCCCTGAGGCGTGCTGGGGGCGCTGCTGTGAAACGC 789
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                              Length 12425;
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Pred. No. 9.5e-09;
0; Mismatches 278;
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SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                            3507 CCGCCGCCGCGCACAGCCGCC 3532
                                                                                                                                                                                                                                                              Sequence 50, Application US/10023523 Patent No. US20020152485A1
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Best Local Similarity 48.6%;
Matches 275; Conservative
                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: Lees, Ann M.
APPLICANT: Lees, Robert S.
APPLICANT: Lew, Simon W.
APPLICANT: Arjona, Anibal A
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; ORGANISM: Homo sapiens
US-10-023-523-50 ,
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Pred. No. 3.2e-08;
0; Mismatches 341; Indels
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US-09-976-740-48
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Fatent No. US2002012938B11
GENERAL INFORMATION:
APPLICANT: Lees, Ann M.
APPLICANT: Lees, Ann M.
APPLICANT: Lees, Robert S.
APPLICANT: Lees, Robert S.
APPLICANT: Lees, Robert S.
TITLE OF INVENTION: PROTIENS AND THEIR USE IN DIAGNOSING AND TREATING
TITLE OF INVENTION: PROTIENS AND THEIR USE IN DIAGNOSING AND TREATING
TITLE OF INVENTION: PROTIENS AND THEIR USE IN DIAGNOSING AND TREATING
TITLE OF INVENTION: PROTIENS AND THEIR USE IN DIAGNOSING AND TREATING
TITLE OF INVENTION: ATHEROSCLEROSIS
FILE REFERENCE: 10797-004001
CURRENT APPLICATION NUMBER: US/10/023,529
CURRENT FILING DATE: 2000-07-14
PRIOR PILING DATE: 2000-03-02
PRIOR APPLICATION NUMBER: US 09/517,849
PRIOR PLILING DATE: 1997-11-26
PRIOR FILING DATE: 1996-11-27
PRIOR PLILING DATE: 1996-11-27
PRIOR PLILING DATE: 1996-11-27
PRIOR APPLICATION NUMBER: US 60/048,547
PRIOR PLILING DATE: 1997-06-03
NUMBER OF SEQ ID NOS: 53
SOPTHARE FRALESCY FOR WINDOWS VERSION 4.0
745
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Pred. No. 3.2e-08;
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US-10-023-529-48
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866 CGTCGCCCCCGGGAGTCGCCGCTGCCGCCGCCGCCGCCGCCGCCGCCGCACAGCA
                                                    379 CAGCTGCGCGTCTGGGGCGCCCCCCGCAACTCTGATCCGGCTCTGGGCTTGGACGAC
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Best Local Simi
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TITLE
JOURNAL
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BI668730
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KEYWORDS
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//lab_host="DH10B (Life Technologies) (TI phage resistant)"
//lab_host="DH10B (Life Technologies) (TI phage resistant)"
//note="Organ: eye; Vector: pT773-Pac (Pharmacia) with a modified polylinker; Site_1: EcoR I; Site_2: Not I;
UI-E-ECO is a subtracted cDNA library constructed
according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand CDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded CDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT773-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tags for this library are: fetal eyes, AGAATCAAGA; lens, CGATTAAGTG; retina, CGGCG; Retina Foveal and Macular, GTCS, RPE and Chorold, ACCTR. This library was created for the program, Gene Discovery in the Visual System, supported by National Bye Institute (NEI)."
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Clone Distribution: Researchers may obtain clones from Research Genetics (www.resgen.com).
                                                                                                                                                                /tissue_type="fetal eyes, lens, eye anterior segment, optic nerve, retina, Retina Foveal and Macular, RPE and Choroid"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 612; DB 14;
Pred. No. 5.7e-270;
                                                                                                          /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="UT-E-E00-ahi:1-14-0-UI"
/clone_lib="UI-E-E00"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
                                                                              Location/Qualifiers
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99.8%;
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L Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: Ggapbs-remail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
CDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki
Toshiyuki and Piero Carninci (RIKEN)
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAMI191 row: h column: 17
High quality sequence stop: 782.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BI668730 784 bp mRNA linear EST 12-SEP-2001 603293168F1 NIH_MGC_96 Homo sapiens cDNA clone IMAGE:5312320 5',
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Craniata; Vertebrata; Euteleostomi;
Catarrhini; Hominidae; Homo.
                           540
                                                                                    998
                                                                                                                  926
                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleoston Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (basea; Lo 784)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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867 GGACCCAGAAGTGCCCCCCCCCATCCCGCCACCAGGACTGCTCCCCGGCCAGCACGTCCAGA
                                                                                    CCAGGTGCCTGCACGCCGCCTCTTGCCACCCTGAGCACTGCCCGGATCCCGTGCACCCTG
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99.7%; Pred. No. 1.4e-246;
ive 0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /tissue_type="hypothalamus"
/lab_host="DH10B"
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/db_xref="taxon:9606"
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/clone_lib="NIH_MGC_96"
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                                                                                                                                                                                                                                                           Length 839,
                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                          52.8%; Score 517; DB 13;
99.7%; Pred. No. 2.2e-226;
11ve 0; Mismatches 2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Contact: Robert Strausberg, Ph.D.
Contact: Robert Strausberg, Ph.D.
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
CDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki
Toshiyuki and Plero Carninci (RKEN)
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incryte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://maqe.llnl.gov
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                         217
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                       218 GCGCTCCTCGCCCGTTCCGCCGGTCAGTGCCCCGAGGTGAGCCGGCGGGGGGGCGGTGCAGG
                                       CGCGGCCGGTAAAGGAGCCCCGGCGCCTAAGCGCAGCGTCTCCGCCCTTGGCTGAGACTG
                                                                                                                     AGGCGCAGGAGGCTGAGGATCAGCAGGCGCGCGTCTGGCGCAGCTGCTGCGCGCGTCTGGG
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Location/Qualifiers
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B1546579
B1546579.1 GI:15433891
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DEFINITION
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ORGANISM
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VERSION
KEYWORDS
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AUTHORS
TITLE
JOURNAL
COMMENT
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Tumor Gene Index
Unpublished (1997)
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BF438085/c
LOCUS
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AUTHORS
TITLE
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KEYWORDS
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E 1 (Bases I to 764)

I (Bases I to 764)

National Institutes of Health, Mammalian Gene Collection (MGC)

(Londatished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-rémail.nih.gov

Tissue Procurement: Miklos Palkovits, M.D., Ph.D.

CDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

Location/Qualifiers

I of Ablance stop: 760.

I of Ablance stop: 760.

Ablance ILM-WAGE: 5314814"

//lab_host="MAMGE: 5314814"

//lab_host="MAMGE: Tham!" Vector: pBluescriptk (modified found fact of fact of the fact in f
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0; Mismatches 3;
  BI669134.1 GI:15583367
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Contact: Robert Strausberg, Ph.D.

Email: cgapbs-rémail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.

Emmert-Buck, M.D., Ph.D.

cDNA Library Preparation: M. Bento Soares, Ph.D.

cDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL, send email to:

info@tmage.llni.gov
Seq primer: -40UP from Gibco
High quality sequence stop: 479.
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(organism="homo sapiens"
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  /note="Organ: lung; Vector: pT773D-Pac (Pharmacia) with a modified polylinker; Plasmid DNA from the normalized library NCL_CGAP_Lus was prepared, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (cloneIDs 1414920-1417991 and 1520904-1522439). Subtraction by Bento Soares and M. Fatima Bonaldo. # 86 t
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NCI-GAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
393 GCGCCCCCCCCCAACTCTGATCCGGCTCTGGGCCTGGACGACCCCGGACGCGCCTGCAG 452
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/tissue_type="linsulinoma" |
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                  information on obtaining
(hinoue@im.wustl.edu)
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UI-E-CL1-afa-a-11-0-UI.rl UI-E-CL1 Homo sapiens cDNA clone
UI-E-CL1-afa-a-11-0-UI 5', mRNA sequence.
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Best Local Similarity 100.0%; Pred. No. 1.2e-212;
Matches 487; Conservative 0; Mismatches 0;
             University Genome Sequencing Center For clone please contact: Dr. Hiroshi Inoue Seq primer: -400P from Gibco High quality sequence stop: 415.

Location/Qualifiers
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1 (Dases 1 to 589)

Melton, D., Brown, J., Kenty, G., Permutt, A., Lee, C., Kaestner, K., Lemishka, I., Scearce, M., Brestelli, J., Gradwoll, G., Clifton, S., Hiller, L., Marran, M., Pape, D., Wylle, T., Marrin, J., Blistain, A., Schmitt, A., Theisiang, B., Ritter, E., Ronko, I., Bennett, J., Cardenas, M., Gibbons, M., McCann, R., Cole, R., Tsagareishvili, R., Williams, T., Endocrine Pancreas Consortium

L Unpublished (2000)

Other_ESTS: ij61a10.y1
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Endocrine Pancreas Consortium
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                                                                                               476 TGCTCCGCGCCCGCCTTGACCCTGCCGCCCTAGCAGCCCCAGCTTGTCCCCGGCGCCCGTCC
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               Length 570;
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Dept of Molecular and Cellular Biology, 7 Divinity ?
                                                      Indels
             Score 504; DB 12; 1
Pred. No. 1.9e-220;
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100.0%; Pred. No. 1...
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Email: dmelton@biohp.harvard.edu
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      Query Match
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KEYWORDS
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740

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Total Sequence (1990)

Total Sequence (1990)

Total Seares, MB

Contact: Soares, MB

Program for Rat Gene Discovery and Mapping

University of Lowa

451 Eckstein Medical Research Building lowa City, IA 52242, USA

Tel: 319 335 9565

Email: msoares@blue.weeg.uiowa.edu

Tissue Procurement: Dr. Gregg Hageman

CDNA Library preparation: Dr. M. Bento Soares, Univeristy of Iowa

CDNA Library Arrayed by: Dr. M. Bento Soares, Univeristy of Iowa

DNA Sequencing by: Dr. M. Bento Soares, Univeristy of Iowa

Clone Distribution: Researchers may obtain clones from Research

Genetics (www.resgen.com).

The following repetitive elements were found in this cDNA

sequence: 95-165, >GC_rishLow_complexity

Seg primer: M13 Reverse.
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Jab_host="DHIOB (Life Technologies) (TI phage resistant)"
/Anche="Organ: eye; Vector: pTT3-Pac (Pharmacia) with a modified polylinker; Site_1: EcoR I; Site_2: Not I; U-E-EVO is a subtracted CONA library constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cONA synthesis was primed
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Bonaldo, M.F., Lennon, G. and Soares, M.B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /tissue_type="fetal eyes, lens, eye anterior segment, optic nerve, retina, Retina Foveal and Macular, RPE and
       181 CGCCCTAGCAGCCCAGCTTGTCCCCGCGCCCGTCCCGGCGGGGGGGCGCTCCGACCCCGGGC 240
                                                                                                                                                                                 CGACGTGGACCCCGAGCTGTTGAGGTACTTGCTGGGACGGATTCTTGCGGGAAGCGCGGA
                                                                                                                                                                                                                                                                                                                                                         741 TGAGCTGCCCCCTGAGGGCGTGCTGGGGGCGCTGCGTGTGAAACGCCTAGAGACCCC
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UI-E-EJO-ahu-d-07-0-UI.rl UI-E-EJO Homo sapiens cDNA clone
UI-E-EJO-ahu-d-07-0-UI 5', mRNA sequence.
                                                                                                                                                                                                                                                         CTCCGAGGGGGGGGCAGCCCCGCGGCGCCGTGCCGCCGACCCACGATGTGGGGCTC
                                                                                                                                                                                                                                                                                   GGCGCCCCCAGGTGCCTGCACGCCCCCTTGCCACCCTGAGCACTGCCCGGATCC 855
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Homo sapiens"
/db_xref="texton:9606"
/clone="Lib=E00-ahu-d-07-0-UI"
/clone_lib="UI-E-E00"
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//organism="Homo sapiens"
//docantsm="Homo sapiens"
//docantsm="Homo sapiens"
//docantsm="Ur-E-Cil-afa-a-11-0-UI"
//clone_lib="Ur-E-Cil-afa-a-11-0-UI"
//clone_lib="Ur-E-Cil"
//tisque_type="adult"
//dab_host="Daylon E. Life Technologies) (TI phage resistant)
//dev_stage="adult"
//dab_host="Daylon E. Life Technologies) (Ti phage resistant)
//docantsmean is eye; Vector: pTT3-Pac (Pharmacia) with a modified polylinker; Site_1: EcoR I: Site_2: Not I;
//Ur-E-Cil is a normalized cDNA library containing the following tissue(s): refina. The library was constructed according to Bonaldo. Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I; and cloned directionally into pTT3-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is CCGCG. This library was created for the program, Gene Discovery in the Visual System, supported by National Eye Institute (NEI): "

78 a 236 c 207 g 78 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: msoares@blue.weeg.ulowa.edu
Tissue Procurement: Dr. Gregg Hageman
CDNA Library preparation: Dr. M. Bento Soares, Univeristy of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, Univeristy of Iowa
DNA Sequencing by: Dr. M. Bento Soares, Univeristy of Iowa
Clone Distribution: Researchers may obtain clones from Research
                                                                                     Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 599)
                                                                                                                                                                                                   Normalization and subtraction: two approaches to facilitate gene
                                                                                                                                                                                                                                                                                                   Contact: Soares, MB
Program for Rat Gene Discovery and Mapping
University of Iowa
451 Eckstein Medical Research Building Iowa City, IA 52242, USA
Tel: 319 335 8250
Fax: 319 335 9565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           381 GCTGCTGCGCGCTCTGGGGCGCCCCCCCGCAACTCTGATCCGGCTCTGGGCTTTGGACGACGA 440
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                                                                                                                                                                               Bonaldo, M.F., Lennon, G. and Soares, M.B.
                                                                                                                                                                                                                                                       Genome Res. 6 (9), 791-806 (1996)
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BM695925.1 GI:19009183
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with an oligo-dr primer containing a Not I site. Double stranded cDNA was ligated to an ECOR I adaptor, digested with Not I, and cloned directionally into pT773-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dr)18 tail. The sequence tags for this library are: fetal eyes, AGAATCAGA; lens, CGATTAGCGA; eye anterior segment, AATGCCGCAT; optic nerve, CCATTAAGTG; retina, CCGCG; Retina Foveal and Macular GTCC; RPE and Choroid, ACCTA. This library was created for the program, Gene Discovery in the Visual System, supported by National Eye Institute (NEI)."
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1 (bases 1 to 593)
Melton, D., Brown, J., Kenty, G., Permutt, A., Lee, C., Kaestner, K., Lemishka, I., Scearce, M., Brestelli, J., Gradwohl, G., Clifton, S., Hillier, L., Marra, M., Pape, D., Wylie, T., Martin, J., Blistain, A., Schmitt, A., Theising, B., Ritter, E., Ronko, I., Bennett, J., Cardenas
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Pred. No. 8.2e-211;
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/Organism=- house sergetter...
/db_xref="taxon:9606"
/clone_lib="Human insulinoma"
/tissue_type="insulinoma"
/lab_host="HulbB (phage-resistant)"
/lab_host="HulbB (phage-resistant)"
/lab_host="BulbB (phage-resis
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,M., Gibbons,M., McCann,R., Cole,R., Tsagareishvili,R., Williams,T., Jackson,Y. and Bowers,Y.
Endocrine Pancreas Consortium
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                                                                                 Unpublished (2000)
Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
Endocrine Pancreas Consortium
Harvard University, Howard Hughes Medical Institute
Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
                                                                                                                                                                                                                                                                                                                     Email: dmelton@biohp.harvard.edu
Library was constructed by Dr. J. Ferrer In vivo mass-excised to
pBluescript SK-by Dr. H. Inoue DNA sequencing by: Washington
University Genome Sequencing Center For information on obtaining is
clone please contact: Dr. Hiroshi Inoue (hinoue@im.wustl.edu)
Seq primer: -40Up from Gibco
High quality sequence stop: 427.
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/organism="Homo sapiens"
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                                                                                                                                                                                                                                                                Tel: 617-495-1812
Fax: 617-495-8557
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Library was constructed by Dr. J. Ferrer In vivo mass-excised to
pBluescript SR. - by Dr. H. Inoue DNA sequencing by: Washington
University Genome Sequencing Center For information on obtaining a
clone please contact: Dr. Hiroshi Inoue (hinoue@im.wustl.edu)
Seq primer: -400P from Gibco
High quality sequence stop: 435.
Location/Qualifiers
1. 601
/ Organism="Homo sapiens"
/ Ab_xref="taxon:9606"
/ Clone="InAAGE:5023128"
/ Clone="InAAGE:5023128"
/ Lab_host="DH10B (phage-resistant)"
/ Lissue type="insulinoma"
/ Lissue type="in
                                                                                                                                          EST 11-MAR-2002
                                                                                                                                                                     id90d01.x1 Human insulinoma Homo sapiens cDNA clone IMAGE:5023128
3' similar to TR:Q9UHG2 Q9UHG2 PROSAAS PRECURSOR. ;, mRNA sequence.
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Please contact Hiroshi Inoue, MD/PhD for further information on this library (Metabolism Division, Permutt Laboratory, Washington University School of Medicine, Box 8127, 660 S Euclid Ave, St. Louis, MO 63110). Note: this is a Washington University Pancreas EST project library. 184 c 237 g 96 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Harvard University, Howard Hughes Medical Institute
Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
MA 02138
                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 601)
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Other_ESTS: 1d90401.y1
Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
Endocrine Pancreas Consortium
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                                                                                                                                                                                                                                                                                                                                          Homo sapiens
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JOURNAL
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BM052768 515 bp mRNA linear EST 12-MAR-2002 ie69907.x2 welton Normalized Human Islet 4 N4-HIS 1 Homo sapiens cDNA clone IMAGE:5672268 3' similar to TR:Q9UHG2 Q9UHG2 PROSAAS PRECUBSOR. ;, mRNA sequence.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (Bases I to 515)
Melton,D., Brown,J., Kenty,G., Permutt,A., Lee,C., Kaestner,K.,
Lemishka,I., Scearce,M., Brestelli,J., Gradwohl,G., Clifton,S.,
Hillart,L., Marra,M., Pape,D., Wylle,T., Martin,J., Blistain,A.,
Schmitt,A., Theising,B., Ritter,E., Ronko,I., Bennett,J., Cardenas,M., Gibbons,M., McCann,R., Cole,R., Tsagareishvill,R., Williams,T.,
Endocrine Pancreas Consortium
Unpublished (2000)
Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
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Library was constructed by Dr. Douglas Melton DNA sequencing by:
Washington University Genome Sequencing Center For Information on
Obtaining a clone please contact: Juliana Brown
(brown@fas.harvard.edu) This sequence now available from the IMAGE
consortium, for clone orders contact: info@image.llnl.gov
High quality sequence stops: 421.
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Harvard University, Howard Hughes Medical Institute
Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
MA 02138
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/db_xref="traon:9606"
/clone="IMAGE:5672268"
/clone_lib="Melton Normalized Human Islet 4
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BM052768.1 GI:16808478
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/note="Organ: Pancreas; Vector: pSPORTI; Site_1: Not 1; Site_2: Sal 1; Starting library constructed using SuperScript Plasmid Library kit (Life Technologies). CDNA made by oligo-dT prinning. Size-selected by column fractionation; average insert size 1.08 kb. Library was amplified once on solid support and plasmid DNA from library was prepared. The library DNA was normalized by method #4 from Bonaldo, Lennon, and Soares 1996 Genome Research 6:791-806: 0.5 microgram single-stranded library plasmid DNA was mixed with 5 micrograms Product representing library inserts and hybridized to an Ecot of 20. Single-stranded (unhybridized) plasmids were isolated by hydroxyapatite chromatography and used to make this
                                                                                                                                                                                                                                 the IMAGE
                                                  Harvard University, Howard Hughes Medical Institute
Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
MA 02138
                                                                                                                                                  Email: dmelton@biohp.harvard.edu
Library was constructed by Dr. Douglas Melton DNA sequencing by:
Washington University Genome Sequencing Center For information on
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                          Klaus H. Kaestner, & Hiroshi Inoue
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/dev_stage="Adult"
/lab_host="DH10B"
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Pred. No. 9.1e-206;
); Mismatches 0;
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High quality sequence stop: 435.
Location/Qualifiers
                                              Endocrine Pancreas Consortium
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                          Contact: Douglas Melton,
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[ (bases 1 to 518)
Melton,D., Brown,J., Kenty,G., Permutt,A., Lee,C., Kaestner,K., Lemishka,I., Scearce,M., Brestelli,J., Gradwohl,G., Clifton,S., Hiller,L., Marra,M., Pape,D., Wylie,T., Martin,J., Blistain,A., Schmitt,A., Theising,B., Ritter,E., Ronko,I., Bennett,J., Cardenas,M., Glòbons,M., McCann,R., Cole,R., Tsagarelshvili,R., Williams,T. Endocrine Pancreas Conscrium
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BM142527 12-MAR-2002 if35d05.x1 Melton Normalized Human Islet 4 N4-HIS 1 Homo sapiens cDNA clone IMAGE:5678265 3' similar to TR:09UHG2 09UHG2 PROSAAS PRECURSOR. ;, mRNA sequence.
BM142527.1 GI:17152594
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Unpublished (2000)
Ochter_ESTS: 1f35d05,yl
Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
Endocrine Pancras Consortium
Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
Endocrine Pancras Consortium
Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
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Fax: 617-495-8517
Exai: 617-495-8557
Exai: 617-495-8557
Exail: dmelton@blohp.harvard.edu
Library was constructed by Dr. Douglas Melton DNA sequencing by:
Washington University Genome Sequencing Center For information on
obtaining a clone please contact: Juliana Brown
(brown@fas.harvard.edu) This sequence now available from the IMAGE
consortium, for clone orders contact: info@image.llnl.gov
Seq primer: -40UP from Gibco
High quality sequence stope: 426.
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Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
MA 02138
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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      1. .562
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/sex="Both"
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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140 GACCCAGAAGTGCCCCCCCCCATCCCGCCACCAGGACTGCTCCCCGCCAGCACGTCCAGAG 81
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NEIBANK: EST analysis and bioinformatics for ocular genomics
Invest. Ophthalmol. Vis. Sci. 41, (2000) In press
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                                                      Query Match 48.2%; Score 472; DB 12; Length 541; Best Local Similarity 100.0%; Pred. No. 9.1e-206; Matches 472; Conservative 0; Mismatches 0; Indels (
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National Eye Institute
6/331, NIH, Bethesda, MD 20892-2740, USA
TTE: 301 402 3452
Fax: 301 496 0078
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Plate: 10 row: f column: 06
Seq primer: -21M13 forward primer (ABI).
Location/Qualifiers
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/organism="Homo sapiens"
/db_xref="taxon:9606"
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/lab_host="EMDH10B"
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BF724971.1 GI:12040882
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Site_2: Sal 1; Starting library constructed using SuperScript Plasmid Library kit (Life Technologies). CDNA made by oligo-dr priming. Size-selected by Column fractionation; average insert size 1.08 kb. Library was prepared once on solid support and plasmid DNA from library was prepared. The library DNA was normalized by method #4 from Bonaldo, Lennon, and Soares 1996 Genome Research 6:791-806; 0.5 microgram single-stranded library plasmid DNA was mixed with 5 micrograms PCR product representing library inserts and hybridized to an Ecot of 20. Single-stranded (unhybridized) plasmids were isolated by hydroxyapatite chromatography and used to make this
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Malton, D. Brown, J., Kentry, G., Permutt, A., Lee, C., Kaestner, K.,
Lemishka, I., Scearce, M., Brestelli, J., Gradwohl, G., Clifton, S.,
Hillier, L., Marra, M., Pape, D., Wylie, T., Martin, J., Blistain, A.,
Schnitt, A., Theising, B., Ritter, E., Ronko, I., Bennett, J., Cardenas,
M., Gibbons, M., McCann, R., Cole, R., Tsagareishvili, R., Williams, T.,
Jackson, Y. and Bowers, Y.
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100.0%; Pred. No. 9.1e-206;
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/note="Organ: Pancreas; Vector: pSPORT1; Site_1: Not 1; Site_2: Sal 1; Starting library constructed using SuperScript Plasmid Library kit (Life Technologies). cDNA made by oligo-dT priming. Size-selected by column fractionation; average insert size 1.08 kb. Library was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             amplified once on solid support and plasmid DNA from the library was prepared. The library DNA was normalized by method #4 from Bonaldo, Lennon, and Soares 1996 Genome Research 6:791-806; 0.5 microgram single-stranded library plasmid DNA was mixed with 5 micrograms PCR product representing library inserts and hybridized to an Ecot of 20. Single-stranded (unhybridized) plasmids were isolated by hydroxyapatite chromatography and used to make this
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ó
                                                                                                                                                                              Email: dmeltonebiohp.harvard.edu
Library was constructed by Dr. Douglas Melton DNA sequencing by:
Washington University Genome Sequencing Center For information on
Obtaining a clone please contact: Juliana Brown
(brown@fas.harvard.edu) This sequence now available from the IMAGE
consortium, for clone orders contact: info@image.llnl.gov
Seq primer: -40UP from Gibco
High quality sequence stop: 427.
                   Endocrine Pañcreas Consortium
Harvard University, Howard Hughes Medical Institute
Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
MA 02138
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5670632"
/clone=lib="Melton Normalized Human Islet 4 N4-HIS
Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
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/dev_stage="Adult"
/lab_host="DH10B"
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Search completed: April 12, 2003, 20:46:19 Job time : 1608 secs

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Copyright (c) 1993 - 2003 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    593429 seqs, 438583890 residues
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

•	Description	Sequence 5, Appli	Sequence 58, Appl	Sequence 1701, Ap	Sequence 71, Appl	Sequence 13, Appl	Sequence 3684, Ap	Sequence 2663, Ap	Sequence 589, App	Sequence 259, App	Sequence 799, App	Sequence 4193, Ap	Sequence 30, Appl	Sequence 2439, Ap	Sequence 24, Appl	Sequence 24, Appl	Sequence 1, Appli	33,		Sequence 126, App
	ID	US-09-803-589-5	US-09-984-271-58	US-09-880-107-1701	US-09-960-352-71	US-09-803-589-13	US-09-983-965-3684	US-09-983-965-2663	US-09-854-133-589	US-09-833-790-259	US-09-917-800A-799	US-09-983-965-4193	US-09-833-790-30	US-09-880-107-2439	US-09-981-876-24	US-09-148-545-24	US-09-754-949-1	US-09-920-923-33	US-09-905-291A-126	US-09-902-853-126
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	Query Match Length DB	979	1050	301	349	1027	342	372	349	349	380	424	464	476	196	196	942	972	1210	1210
æ	Query Match	100.0	59.6	23.1	3.3	3.3	5.6	2.0	1.9	1.9	1.9	1.9	1.9	1.9	1.9	1.9	1.9	1.9	1.9	1.9
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Length 979; Indels 0

Query Match 100.0%; Score 979; DB 10; Best Local Similarity 100.0%; Pred. No. 0; Matches 979; Conservative 0; Mismatches 0;

Sequence 126, App Sequence 126, App Sequence 311, App Sequence 311, App Sequence 311, App Sequence 311, App Sequence 126, App Sequence 126, App Sequence 126, App Sequence 311, App Sequence 311, App Sequence 311, App Sequence 311, App Sequence 311, App Sequence 311, App Sequence 126, App	THERAPEUTIC AND OTHER	
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3-09-984-271-58 Sequence 58, Application US/09984271

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         466 GCTCGCGCTCTGCTCCGCGCCCCTTGACCCTGCCGCCCTAGCAGCCCAGCTTGTCCCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   646 TACTIGCIGGGACGGATTCTIGCGGGAAGCGCGGACTCCGAGGGGGTGGCAGCCCCGCGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            639 TACTTGCTGGGACGGATTCTTGCGGGGAAGCGCGGACTCCGAGGGGGGTGGCAGCCCCGCGC
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Pred. No. 1.6e-282;
0; Mismatches 1;
PUBLICATION NO. US20030040088A1
GENERAL INFORMATION:
TATLE ROSON et al.
TITLE OF INVENTION: 71 Human Secreted Proteins
FILE REFERENCE: PZ030P1
CURRENT APPLICATION NUMBER: US/09/984,271
CURRENT FILING DATE: 2001-10-29
FRIOR APPLICATION NUMBER: 09/482,273
FRIOR APPLICATION NUMBER: 09/482,273
FRIOR APPLICATION NUMBER: 06/092,921
FRIOR APPLICATION NUMBER: 60/092,921
FRIOR APPLICATION NUMBER: 60/092,921
FRIOR APPLICATION NUMBER: 60/092,922
FRIOR FILING DATE: 1998-07-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   939 CAGCCCTCTCACCCGAGGATCCCTACCCCCTGGC 972
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Best Local Similarity 99.8%;
Matches 633; Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-984-271-58
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PATENT NO. USJOUZOLIZZIALI

PATENT NO. USJOUZOLIZZIALI

APPLICANT: HOLEAMAN, Douglas A.

TITLE OF INVENTION: PROGNOSTIC, DIAGNOSTIC, PREVENTIVE, THERAPEUTIC AND OTHER

TITLE OF INVENTION: USES

FILE REFERENCE: 0734 - 325001

CURRENT FILING DATE: 1098 - 08 - 04

PRIOR APPLICATION NUMBER: US 60/054, 645

PRIOR FILING DATE: 1997 - 08 - 04

PRIOR FILING DATE: 1997 - 08 - 06

PRIOR FILING DATE: 1997 - 08 - 06

PRIOR PILING DATE: 1997 - 08 - 06

PRIOR FILING DATE: 1997 - 08 - 06

PRIOR PILING DATE: 1997 - 08 - 06

PRIOR FILING DATE: 1997 - 09 - 01

PRIOR FILING DATE: 1997 - 09 - 01

PRIOR FILING DATE: 1997 - 09 - 01

PRIOR FILING DATE: 1999 - 09 - 01

PRIOR APPLICATION NUMBER: US 60/058, 108

PRIOR FILING DATE: 1999 - 09 - 01

PRIOR PILING DATE: 1999 - 09 - 01

PRIOR PILING DATE: 1999 - 09 - 01

PRIOR FILING DATE: 1999 - 09 - 01

PRIOR FILING DATE: 1999 - 09 - 01

PRIOR PILING DATE: 1999 - 09 - 01

PRIOR PILING DATE: 1999 - 09 - 01

PRIOR FILING DATE: 1999 - 09 - 01

PRIOR PILING DATE: 1999 - 09 - 01
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APPLICANT: Tao, Nengbing
APPLICANT: Tao, Nengbing
APPLICANT: Byatt, John C.
TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION
FILLE PREPERENCE: 37-21(10297)C
CURRENT APPLICATION NUMBER: US/09/983,965
CURRENT FILLING DATE: 2001-10-26
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                                                DB 10; L
1.6e-06;
thes 0;
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1.3e-06;
                                                3.3%; Score 32; DB
100.0%; Pred. No. 1.6
iive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 3.3%; Score 32; DB Best Local Similarity 100.0%; Pred. No. 1.3 Matches 32; Conservative 0; Mismatches
                                                                                                                                                      352 GAGGATCAGCAGGCGCGCGTCCTGGCGCAGCT 383
                                                                                                                                                                                 80
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US-09-983-965-3684
Sequence 3684, Application US/09983965
Patent No. US/20020137160A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                     Sequence 13, Application US/09803589 Patent No. US20020112251A1
                                     Ouery Match
Best Local Similarity 100.0
Matches 32; Conservative
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; LOCATION: (106)...(630)
US-09-803-589-13
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                                                                                                                                                                                                                                                                                     RESULT 5
US-09-803-589-13
US-09-960-352-71
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APPLICANT: Tailor, Neighing
APPLICANT: Mathialagan, Nagapan
TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
TITLE OF INVENTION: NUCLEIC ACID AND STATE OF INVENTION: NUCLEIC ACID AND FAIT DEPOSITION
FILE REFERENCE: 16511.006/37-21(10298)C
CURRENT APPLICATION NUMBER: US/09/960,352
CURRENT FILING DATE: 2001-09-24
NUMBER OF SEQ ID NOS: 15112
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         241 CTGGGGGGCGCTGCTSCGTGTGAACGCCTAGAGACCCCGGGGCGCCCCAGGTGCCTGCACGC 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   181 CGCCTCTTGCCACCCTGAGCACTGCCCGGATCCCGTGCACCCTGGGACCCAGAAGTGCCC 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               703 CGCCGCCTCCGCCGTGCCGCCGACCACGATGTGGGGCTCTGAGCTGCCCCCTGAGGGCGTG 762
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  763 CTGGGGGCGCTGCTGCGTGTGAAACGCCTAGAGACCCCGGCGCCCCAGGTGCCTGCACGC 822
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      823 CGCCTCTTGCCACCCTGAGCACTGCCCGGATCCCGTGCACCCTGGGACCCAGAAGTGCCC 882
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         883 CCGCCATCCCGCCACCAGGACTGCTCCCCGCCAGCACGTCCAGAGCAACTTACCCCGGCC 942
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                                                                                                                                      ; OTHER INFORMATION: Genbank Accession No. US20020142981A1 D59847 US-09-880-107-1701
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ORGANISM: Bos taurus
OTHER INFORMATION: Clone ID: 01-LIB3057-002-Q1-K1-A9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 226; DB 10;
Pred. No. 1.2e-103;
0; Mismatches 1;
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                                                             Sequence 1701, Application US/09880107
Patent No. US20020142981A1
GENERAL INFORMATION:
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Patent No. US20020137139A1
GENERAL INFORMATION:
APPLICANT: Warren, Wesley C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 23.1%;
Best Local Similarity 99.6%;
Matches 276; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA
ORGANISM: Homo sapiens
                                                US-09-880-107-1701/c
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US-09-960-352-71
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APPLICANT: Indirias, Carol Y.
APPLICANT: Indirias, Carol Y.
APPLICANT: End. Ligun
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: COMPOSITIONS OF LUNG CANCER
FILE REFERENCE: 210121.512
CURRENT APPLICATION NUMBER: US/09/833,790
CURRENT FILING DATE: 2001-04-11
NUMBER OF SEQ ID NOS: 440
SOFTWARE: FEASESEQ for Windows Version 4.0
SEQ ID NO 259
LENGTH: 349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1.9%; Score 19; DB 10; Length 349;
100.0%; Pred. No. 5.2;
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5.2;
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APPLICANT: Johnson, Kory
APPLICANT: Castle, Arthur
APPLICANT: Castle, Arthur
APPLICANT: Gene Logic, Inc.
TITLE OF INVENTION: Molecular Toxicology Modeling
FILE REFERENCE: 44921-5038-US
CURRENT APPLICATION NUMBER: US/09/917,800A
CURRENT FILING DATE: 2001-07-31
                                                                                                                                                                                                                                                                                                              Mismatches
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      NUMBER OF SEQ ID NOS: 735
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 589
LENCTH: 349
                                                                                                                                                                                                                                                Score 19;
Pred. No.
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PRIOR FILING DATE: 2000-07-31
PRIOR APPLICATION NUMBER: US 60/222,880
PRIOR FILING DATE: 2000-11-02
PRIOR APPLICATION NUMBER: US 60/290,029
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US 60/290,029
APPLICATION NUMBER: US 60/290,029
APPLICATION NUMBER: US 60/290,645
FILING DATE: 2001-05-15
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Patent No. US20020068288A1
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100.0%; Pre
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100.0%; Pr.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Lodes, Michael J. APPLICANT: Wang, Tongtong APPLICANT: Secrist, Heather
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 1.9
Best Local Similarity 100.
Matches 19; Conservative
                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                           ; TYPE: DNA; ORGANISM: Homo sapiens
US-09-854-133-589
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA
ORGANISM: Homo sapiens
US-09-833-790-259
                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 19; Conserv
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US-09-917-800A-799/c
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Patent No. US20020137160A1

GAPLICANT: HTDORMATION:
APPLICANT: Marren, Wesley C.
APPLICANT: Tao, Nengbing
APPLICANT: Byatt, John C.
APPLICANT: Byatt, John C.
APPLICANT: Mathialagan, Nagappan
TITLE OF INVENTION: MUCLEIC ACID AND CTHER MOLECULES ASSOCIATED WITH LACTATION AND
FILE OF INVENTION: MUSCLE AND FAT DEPOSITION
FILE OF INVENTION: MUSCLE AND FAT DEPOSITION
FILE OF INVENTION: MUSCLE AND FAT DEPOSITION
FILE PREFERENCE: 37-21(10297)C
CURRENT APPLICATION NUMBER: US/09/983,965
CURRENT FILING DATE: 1999-12-15
PRIOR APPLICATION NUMBER: US 60/113,678
PRIOR FILING DATE: 1999-12-17
NUMBER OF SEQ ID NOS: 5912
SEQUENCE OF SEQUENCE SET OF SEQUENCE SEQUENCE SEQUENCE SET OF SEQUENCE SEQUEN
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APPLICANT: Lodes, Michael J.
APPLICANT: Mohamath, Raodoh
APPLICANT: Henderson, Robert A.
APPLICANT: Benson, Darin R.
APPLICANT: Secrist, Heather
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
TITLE OF INVENTION: THE THERAPY AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.475c10
CURRENT APPLICATION NUMBER: US/09/854,133
CURRENT FILING DAIE: 2001-05-11
                                                                                                                                                                                                                                                                                                                                                                                        2.6%; Score 25; DB 10; Length 342;
100.0%; Pred. No. 0.0051;
tive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                 ; OTHER INFORMATION: Clone ID: 43-LIB3058-043-Q1-K1-C12 US-09-983-965-3684
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100.0%; Pred. No.
tive 0; Mismatc
PRIOR APPLICATION NUMBER: US 09/465,231
PRIOR FILING DATE: 1999-12-15
PRIOR APPLICATION NUMBER: US 60/113,678
PRIOR FILING DATE: 1998-12-17
SEQ ID NO 3684
LENGTH: 342
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. Sequence 589, Application US/09854133
. Publication No. US20020183499A1
. GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     25; Conservative
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                                                                                                                                                                                                              TYPE: DNA
ORGANISM: Bos taurus
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA ORGANISM: Bos taurus
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Best Local Similarity
Matches 20; Conserv
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US-09-983-965-2663
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Sequence 2431.75

Patent No. US20020142981A1

GENERAL INFORMATION:

APPLICANT: Horne, Darci T.

APPLICANT: Vockley, Joseph G.

APPLICANT: Gene Logic, Inc.

TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer FILE REFERENCE: 44921-508-W0

CURRENT APPLICATION NUMBER: US/09/880,107

CURRENT FILING DATE: 2001-06-14

PRIOR FILING DATE: 2000-06-14

PRIOR SPELICATION NUMBER: US 60/237,054

PRIOR APPLICATION NUMBER: US 60/237,054

SPRIOR SELING DATE: 2000-06-14

SPRIOR SELING DATE: 2000-10-02

NUMBER OF SEQ. ID NOS: 3950

SOFTWARE: Patentin Ver. 2.1
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                                                APPLICANT: Fan, Liqun
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FULLE REFERENCE: 210121.512
CURRENT APPLICATION NUMBER: US/09/833,790
CURRENT FILING DATE: 2001-04-11
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Fatent No. US20020164669A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITE OF INVENTION: 70 Human Secreted Proteins
FILE REFERENCE: PZ001P1
CURRENT APPLICATION NUMBER: US/09/981,876
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                                                                                                                                                                                    NUMBER OF SEQ ID NOS: 440
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 30
LENGTH: 464
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100.0%; Pred. No.
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LOCATION: (1)..(476)
OTHER INFORMATION: n = a or c or g or t
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100.0%; Pre
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Matches 19; Conservative
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; ORGANISM: Homo sapien
US-09-833-790-30
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Matches 19; Conserv
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LENGTH: 476
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APPLICANT: Tao, Nengbing
APPLICANT: Tao, Nengbing
APPLICANT: Tao, Nengbing
APPLICANT: Byatt, John C.
APPLICANT: Mathialagan, Nagappan
TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION
FILE REPERENCE: 37-21(1029);
CURRENT APPLICATION NUMBER: US 09/465,231
PRIOR FILING DATE: 1999-12-15
PRIOR FILING DATE: 1999-12-15
PRIOR FILING DATE: 1998-12-17
NUMBER OF SEQ ID NOS: 5912
SEQ ID NO 4193
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US-09-983-965-4193
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PRIOR APPLICATION NUMBER: US 60/292,336
PRIOR FILING DATE: 2001-05-22
PRIOR PILING DATE: 2001-05-36
PRIOR PILING DATE: 2001-06-06
PRIOR FILING DATE: 2001-06-10
PRIOR FILING DATE: 2001-06-13
PRIOR PLICATION NUMBER: US 60/298,884
PRIOR FILING DATE: 2001-06-19
PRIOR PLILING DATE: 2001-06-19
PRIOR PLILING DATE: 2001-00-19
PRIOR PLILING DATE: 2001-00-19
PRIOR PLILING DATE: 2001-07-09
NUMBER OF SEQ ID NOS: 1740
SOFTWARE: PatentIn Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 19;
Pred. No.
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. Sequence 30, Application US/09833790
. Patent No. US20020068288A1
. GENERAL INFORMATION:
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Best Local Similarity 100.0%; P
Matches 19; Conservative 0;
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                                                                                                                                                                                                                                                                                                                      TYPE: DNA ORGANISM: Rattus norvegicus
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LENGTH: 380
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APPLICANT:
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E: 2001-10-19 NUMBER: 09/148,54 NUMBER: 09/040,16 1997-03-07 NUMBER: 60/040,33 1997-03-07 NUMBER: 60/040,16 1997-03-07 NUMBER: 60/040,62 1997-03-07 NUMBER: 60/040,62 1997-03-07 NUMBER: 60/040,62 1997-03-07 NUMBER: 60/040,63 NUMBER: 60/040,63	NUMBER: 60	. M . M . M . M . M . M . M . M . M . M
NT FILING APPLICATI FILING DA APPLICATI	APPLICADION APPLICATION APPLICATION FILING DATE APPLIC	FILING DATE: APPLICATION
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PRIOR APPLICATION NUMBER: 60/043,671
PRIOR APPLICATION NUMBER: 60/043,674
PRIOR PILING DATE: 1997-04-11
PRIOR PILING DATE: 1997-06-22
PRIOR APPLICATION NUMBER: 60/056, 899
PRIOR PILING DATE: 1997-06-22
PRIOR APPLICATION NUMBER: 60/056, 819
PRIOR PILING DATE: 1997-06-22
PRIOR

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R FILING DATE: 1997-05-23

R APPLICATION NUMBER: 60/047,618

R FILING DATE: 1997-05-23

R APPLICATION NUMBER: 60/047,503

R FILING DATE: 1997-05-23

R APPLICATION NUMBER: 60/047,592

R APPLICATION NUMBER: 60/047,592

R APPLICATION NUMBER: 60/047,581

R R PLING DATE: 1997-05-23
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R APPLICATION NUMBER: 60/047,492
R FILING DATE: 1997-05-23
R APPLICATION NUMBER: 60/047,598
R FILING DATE: 1997-05-23
R APPLICATION NUMBER: 60/047,613
R APPLICATION NUMBER: 60/047,582
R R PILING DATE: 1997-05-23
R R PILING DATE: 1997-05-23
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R FILING DATE: 1997-04-11
R APPLICATION NUMBER: 60/043,568
R FILING DATE: 1997-04-11
R APPLICATION NUMBER: 60/043,314
R FILING DATE: 1997-04-11
R APPLICATION NUMBER: 60/043,569
R FILING DATE: 1997-04-11
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R APPLICATION NUMBER: 60/047,502

R PILING DATE: 1997-05-23

R RPILICATION NUMBER: 60/047,633

R FILING DATE: 1997-05-23

R R FILING DATE: 1997-05-23

R FILING DATE: 1997-05-23

R FILING DATE: 1997-05-23

R APPLICATION NUMBER: 60/047,583
                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: 60/047,615
FILING DATE: 1997-05-23
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APPLICATION NUMBER: 60/047,632
                                                                                                                                       FILING DATE: 1997-03-07
APPLICATION NUMBER: 60/040,334
                                                                                                                                                                                                                             FILING DATE: 1997-03-07
APPLICATION NUMBER: 60/040,336
                                                                                                                                                                                                                                                                                                                   FILING DATE: 1997-03-07
APPLICATION NUMBER: 60/040,163
FILING DATE: 1997-03-07
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FILING DATE: 1997-04-11
APPLICATION NUMBER: 60/043,671
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APPLICATION NUMBER: 60/043,674
FILING DATE: 1997-04-11
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APPLICATION NUMBER: 60/047,601
FILING DATE: 1997-05-23
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100.0%; Pred. No. 4.3;
ive 0; Mismatches 0; Indels
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PUblication No. US20030027132A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TILLE OF INVENTION: 70 Human Secreted Proteins
TILLE OF INVENTION: 70 Human Secreted Proteins
CURRENT APPLICATION NUMBER: US/09/148,545
CURRENT FILING DATE: 1998-09-04
BARLIER FILING DATE: 1998-03-06
EARLIER FILING DATE: 1998-03-06
BARLIER APPLICATION NUMBER: 60/040,162
BARLIER APPLICATION NUMBER: 60/040,163
BARLIER APPLICATION NUMBER: 60/040,163
BARLIER APPLICATION NUMBER: 60/040,163
BARLIER APPLICATION NUMBER: 60/040,333
RELIGIO DATE: 1997-05-23

RAPPLICATION NUMBER: 60/047,594

RELING DATE: 1997-05-23

RELING DATE: 1997-05-23

RELING DATE: 1997-05-23

REPLING DATE: 1997-05-23

RELING DATE: 1997-05-23

RELING DATE: 1997-05-23

RELING DATE: 1997-05-23

RELING DATE: 1997-04-11

RELING DATE: 1997-06-23

RELING DATE: 1997-06-22

REPLING DATE: 1997-06-22

RE
PRIOR FILING DATE: 1997-05-29
PRIOR APPLICATION NUMBER: 60/0
PRIOR PLING DATE: 1997-05-23
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PRIOR PLING DATE: 1997-04-11
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PRIOR PLING DATE: 1997-04-11
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Best Local Similarity 100.
Matches 19; Conservative
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EARLIER APPLICATION NUMBER: 090-08-22

EARLIER FILING DATE: 1997-08-22

EARLIER PELICATION NUMBER: 60/056,877

EARLIER FILING DATE: 1997-08-22

EARLIER FILING DATE: 1997-08-22
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R APPLICATION NUMBER: 60/056,880

R APPLICATION NUMBER: 60/056,894

R FILING DATE: 1997-08-22

R APPLICATION NUMBER: 60/056,911

R FILING DATE: 1997-08-22

R APPLICATION NUMBER: 60/056,911

R FILING DATE: 1997-08-22

R APPLICATION NUMBER: 60/056,636

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R APPLICATION NUMBER: 60/056,636
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RR APPLICATION NUMBER: 60/056,882
RR APPLICATION NUMBER: 60/056,637
RR FILING DATE: 1997-08-22
RR APPLICATION NUMBER: 60/056,903
RR FILING DATE: 1997-08-22
RR FILING DATE: 1997-08-28
RR FILING DATE: 1997-08-28
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TR APPLICATION NUMBER: 60/056,878
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TR APPLICATION NUMBER: 60/056,872
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R FILING DATE: 1997-08-22
R APPLICATION NUMBER: 60/056,864
R APPLICATION NUMBER: 60/056,631
R FILING DATE: 1997-08-22
R APPLICATION NUMBER: 60/056,845
                                                                                                                        EARLIER FILING DATE: 1997-04-11
EARLIER APPLICATION UNBER: 60/048,974
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/056,886
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,877
EARLIER FILING DATE: 1997-08-22
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APPLICATION NUMBER: 60/056,879
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FILING DATE: 1997-05-23
APPLICATION NUMBER: 60/057,761
FILING DATE: 05-Sep-1997
APPLICATION NUMBER: 60/047,599
PLICATION NUMBER: 60/043,313
                                              APPLICATION NUMBER: 60/043,672
                                                                    EARLIER FILING DATE: 1997-04-11
EARLIER APPLICATION NUMBER: 60/043,315
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APPLICATION NUMBER: 60/056,892
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Search completed: April 12, 2003, 21:41:32 Job time : 162 secs

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April 4, 2003, 14:15:09 ; Search time 18 Seconds (without alignments) 1388.608 Million cell updates/sec
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GenCore version 5.1.4\_p5\_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 2000000000
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1: pir1:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	translation initia		_				hypothetical prote	probable exonuclea	probable dihydroli	glial growth facto	immediate-early pr			polyprotein	Xin protein, stage	ETS2 repressor fac	probable ATP-bindi	probable multi-dom	TonB-dependent rec	precorrin-3 methyl	protein kinase, tr	UL36 protein - hum	cycH protein - Par	progesterone recep	protein phosphatas	smc protein [impor	GTP-binding regula	>	
SUMMARIES	QI	B97369	AB2587	C75318	G87485	T33110	B56708	T29018	T03465	T35297	S32357	EDBEIF	EDBE75	A45344	FOLJLK	T14267	S59133	T35745	T37057	G87389	F83283	T36663	WMBEH6	S61305	QRHUP	T03852	D87295	S52418	œ	S37671
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de	Query Match	11.1	11.1	10.2	6,6	9.7	9.4	9.3	9.3	9.5	9.1	9.1	0.6	8.9	6.8	8.8	8.8	8.8	8.7	9.0	9.	8.0	9.6	8.5	8	8.5	8.5	8.4	8.4	4.4
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translation initiation factor IF-2 [imported] - Agrobacterium tumefaciens (strain C58 C; Species: Agrobacterium tumefaciens C; Deteches: Agrobacterium tumefaciens C; Date: 11-Jan-2002 #sequence\_revision 11-Jan-2002 #text\_change 01-Feb-2002 C; Accession: AB2587

RESULT 2 AB2587

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) א <i>ו</i>	Goodner A.; Liu,	ner, iu, F	B.; Wollam,	nkle, lam,	B.; Hinkle, G.; Gattung, F.; Wollam, C.; Allinger,	attu ling	ng, er,	S.; Miller, N.; I M.; Doughty, D.;	Blanchard Scott, C	, M.;	10, C.;	B.; Goldm Markelz,	dg ,
ייהומיג	A;Title: A;Refere	e: Geno erence n	Science 294, 2323-2328, 200 A,Title: Genome Sequence of A,Reference number: A97359,	-2328 equer r: AS	-	the PMID	Pla:	t Pathogen and 43194	Biotechnology	ogy Agent		Agrobacterium	E
. ~ ~ ~ ~	), Stat ), Mole ), Resi	us: p cule dues:	A; Status: preliminary A; Molecule type: DNA A; Residues: 1-913 <ku A; Cross-references: G</ku 	Inary DNA S <kur></kur>	y UR> GB:AE007869	869;		PIDN:AAK85907.1; PI	PID:9151549	54;	GSPDB:GN0016	69	
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u	οy	187 T	PDVDPE	LLRYI	LLGRILA	GSAD	SEG	TPDVDPELLRYLLGRILAGSADSEGVAAPRRLRRAADHD	:	-VGSELPPEGVLGAL	239		
Ц	qq	1 232 T	111 TPD				7		III GAVRRGSSL	 PARG	264		
J	Οy	240 L	RVKRLE	TPAPC	LRVKRLETPAPQVPARRL	257							
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Qy 54 GAPRETRESVPRGEAAGAVQELARALAHLLEAERQERARAEAQEAEDQGAR 104	RESULT 4 (89748 (1970)	Ouery Match Best Local Similarity 29.8%; Pred. No. 0.22; Best Local Similarity 29.8%; Pred. No. 0.22; Matches 82; Conservative 15; Mismatches 91; Indels 87; Gaps  Qy 45 AASPPLAETGAPRFFRSVPRGEAGAVGELARAL-AHLLEAERGERARA	OY 144 RLDPAALAAQLVPAAVPAAALRPPPVYDDGPAGPDAEEAGDETPDVDPEL-LRY 197	RESULT 5 T33110 hypotherical protein C18H7.3 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 21-Jan-2000 C;Accession: T33110 R;Tin-Wollam, A.; Fronick, W. submitted to the EMBL Data Library, May 1998 A;Description: The sequence of C. elegans cosmid C18H7. A;Reference number: Z21284
R; Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, I erage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; McClell; Science 294, 2317-2323, 2001 A; Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm, ster, E.W. A; Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58. A; Reference number: AB2587 A; Reference number: AB2577; PMID:11743193 A; Reference number: AB2587 A; Residues: 1-913 < CUR> A; Residues: GB: AE008688; PIDN: AAL41112.1; PID:g17738404; GSPDB:GN00186 C; Genetics: A; Gene: infb A; Men position: circular chromosome A; Monorfailion: circular chromosome A; Monorfailion: circular chromosome C; Superfamily: translation intiation factor IP-2: translation closures	Query Match  11.1%; Score 146; DB 2; Length 913;  Best Local Similarity 25.2%; Pred. No. 0.034;  Matches 65; Conservative 34; Mismatches 79; Indels 80; Gaps 12;  29 PPALCARPVKEPRGLSAASPPLAETGAPRRFRRSVPRGEAAGAV 72	2000	Circlession: C7318  M.; Shen, M.; Vamathevan, J.J.; Lam, P.; Michey, E.K.; Peterson, J.D.; Dodson, R.J.; M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; Ma S.; Smith, H.O.; Venter, J.C.; Fraser, C.M. Science 286, 1571-1577, 1999  A; Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1. A; Accession: C7518 A; Residues: 1-553 < WHI> A; Cross-references: GB: AE002044; GB: AE000513; NID: g6459872; PIDN: AAF11639.1; PID: g645988	A; Gene: DR2090 A; Map position: 1 Query Match Best Local Similarity 25.0%; Pred. No. 0.12; Matches 70; Conservative 24; Mismatches 108; Indels 78; Gaps 11; Qy 24 GLEREPPRALCARPVKEPRGLSAASPP

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.; Nelson, K.E.; Eisen, J.; Heidelberg, ckin, A.S.; Gwinn, M.L.; Haft, D.H.; Ko., Shapiro, L.; Venter, J.C.; Fraser, C. crescentus.
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AALLRARLDPAALAAQ---LVPAP 158
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SAAPARQVQERSTATQTQVIQAAP 204
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A;Residues: 1-815 <ZHO>
A;Residues: 1-815 <ZHO>
A;Residues: 1-815 <ZHO>
A;Residues: 1-815 <ZHO>
CSCOSS-references: GB:U25278; NID:9837260; PIDN:AAA81381.1; PID:9837261
C;Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homolog C;Reywords: ATP
F;52-315/Domain: protein kinase homology <KIN>
F;60-68/Region: protein kinase ATP-binding motif
                        A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA

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C; Species: Homo sapiens (man)
C; Species: Homo sapiens (man)
C; Date: 19-0ct-1995 #sequence_revision 19-0ct-1995 #text_change 24-Sep-1999
C; Accession: B56708
R; Zhou, G.; Bao, Z.Q.; Dixon, J.E.
J. Biol. Chem. 270, 12665-12669, 1995
A; Title: Components of a new human protein kinase signal transduction pathway. A; Reference number: A56708; MUID:95279403; PMID:7759517
A; Accession: B56708
A; Status: preliminary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RA--RLDPAALAAQLVPAPVPAAALRPRPPVYDDGPAGPDAEEAGDETPDVDPELLRYLL 199
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9.4%; Score 124.5; DB 2; Length
Best Local Similarity 22.7%; Pred. No. 0.76;
Matches 67; Conservative 31; Mismatches 116; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 9.7%; Score 127.5; DB 2; Similarity 30.0%; Pred. No. 0.27; 54; Conservative 10; Mismatches 84;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          200 GRILAGSADSEGVAAPRRLRRAADHDVGSELPP 232
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----GGAEPAG-AAPEAAAAPEGAGGGEAPP 441
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A; Accession: T33110
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Best Local S
Matches 64
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A;Map position: 2
A;Introns: 22/2; 45/3; 108/1
C;Superfamily: collagen alpha 1(I) chain; fibrillar collagen carboxyl-terminal homolo
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C; Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 02-Jun-2000
C; Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 02-Jun-2000
C; Accession: T03465
R; Vlock, C.; Paces, V.; Maltsev, N.; Paces, J.; Haselkorn, R.; Fonstein, M.
Proc. Natl. Acad. Sci. U.S.A. 94, 9384-9388, 1997
A; Feiference of a 189-kb segment of the chromosome of Rhodobacter capsulatus SB1
A; Reference number: 214955; MUID:97404404; PMID:9256491
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C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: EMBL:U23181; PIDN:AAC48204.1; GSPDB:GN00020; CESP:ZK84.1 A; Experimental source: strain Bristol N2; clone ZK84 C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                   hypothetical protein zx84.1 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Taylous
B;Kirsten, J.
Submitted to the EMBL Data Library, April 1995
A;Description: The sequence of C. elegans cosmid zx84.
A;Reference number: Z20553
A;Accession: T29918
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                                                                              : ||| : |:|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |-|| : |
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Live 14; Mismatches 107; Indels
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214 APRRLRRAADHDVGSELPPEGVLGALLRVKRLETPAPQ----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Status: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: DNA A;Residues: 1-801 <KIR>
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A;Molecule type: DNA
A;Residues: 1-1238 <VLC>
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C; Superfamily: chromosome segregation protein SMC1
C; Keywords: DNA repair; exonuclease; hydrolase
                                                                                                                     ----PAPHPTGPPGP----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 28.5%
Matches 73; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            235 VLGALLRVKRLETPAP 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 725 PAAP-----ETPAP 733
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Ma	Query Match 9.3%; Score 123; DB 2; Length 1238; Best Local Similarity 26.5%; Pred. No. 1.4; Matches 85; Conservative 18; Mismatches 114; Indels 104; Gaps 16;	OY 249 APOVPARRILP 259 Db 335 APAPARKEN 345
oy ob	8 WGPRAGGVGLLVLLLLGLFRP-PPALCARPVKEPRGLSAASPPLAETGAPRRFRSV 63	SULT 10
Oy D	OQARVLAQLL           : AQEAALAEAR	\$32357
oy op	111 RVWGAPRNSDPALGLDDDPDAP	<pre>C;Accession: S32357 R;Marchionni, M.A.; Goodearl, A.D.J.; Chen, M.S.; Bermingham-McDonogh, O.; Kirk, C.; les, I.; Davis, J.B.; Hsuan, J.J.; Totty, N.F.; Otsu, M.; McBurney, R.N.; Waterfield, Nature 362, 312-318, 1993</pre>
oy Op	137 ARALLRARLDPAALAAQLVPAPVPAAALR-PRPPVYDDGPAGPD	A;Title: Glial growth factors are alternatively spliced erbB2 ligands expressed in th A;Reference number: S32357; MUID:93205115; PMID:8096067 A;Accession: S32357 A;Status: preliminary
Oy Dp	180 AEEAGDETPDVDPELLRYLLGRILAGSADSEGVAAPRRLRRAADHDVGSELPPEGVLGAL 239   1	A; Molecule type: mRNA A; Residues: 1-422 < CAMR> A; Residues: 1-422 < CAMR> A; Cross-references: GB:L12260; NID:g292047; PIDN:AAB59622.1; PID:g292048 C; Superfamily: human heregulin; EGF homology E: 363.4.02 Anomain: man heregulin; energy
Oy Dp	240 LRVKRLETPAPQVPARRLLPP 260 1	Query Match  Query Match  Best Local Similarity 28.0%; Pred. No. 0.82;  Matches 56; Conservative 15; Mismatches 66; Indels 63; Gaps 9;
RESULT T35297 probab	RESULT 9 135297 probable dihydrolipoamide S-succinyltransferase (EC 2.3.1.61) SC5F7.20 [similarity] - St	OY 2 AGSPLLWGPRAGGVGLLVLLLLGLFRPPPALCARPVKEPRGLSAASP 48
C; Sr C; Da	scies: Streptomyces coelicolor .e: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 08-Sep-2000 .ession: T35297	49 PLAETGAPREFR 
A; Se A; Re A; Ac	egger, K.; Harris, D.; Bentley, S.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.     the definition of the common of the c	DD 67 PSVGSVQELAQRAAVVIEGKVHPQRRQQGALDRKAAAAAG 106 Qy 109 LLRVWGAPRNSDPALGLDDDPDAPAAQLARALLRARLDPAALAAQLVPAPVPAAALRPRP 168
A; St A; Mo	ttus: translated from GB/EMBL/DDBJ lecule type: DNA idnes: 1-590 csFE>	107
A; Ex	osseria 2015 - 2	UY 109 FVILLOGRAGIDER 188   :                   Db 141 PSWPTAPV-PSAGEPGEEAP 159
CC; SCC CC; SCC CC; Ke F; F F; F F F; F F F F F F F F F F F F	A; Gene: sucB; SCOEDB:SC5F7.20 C; Superfamily: Mycobacterium probable dihydrolipoamide succinyltransferase; lipoyl/biotil C; Keywords: acyltransferase; coenzyme A: F; 4-77/Domain: lipoyl/biotin-binding homology <lpb1> F; 4-77/Domain: lipoyl/biotin-binding homology <lpb2> F; 31.170/Abnding site: lipomide (Lys) (covalent) #status predicted F; 43.730/Abnding site: lipomide (Lys) (covalent) #status predicted</lpb2></lpb1>	RESULT 11 EDBEIF Immediate-early protein IE180 - suid herpesvirus 1 (strain Indiana-Funkhauser) C; Species: suid herpesvirus 1 C; Date: 30-7un-1900 #sequence_revision 30-Jun-1990 #text_change 16-Feb-1997
F; 17	//////////////////////////////////////	C;Accession: S04/13 C;Cheung, A.K. Nucleic Acids Res. 17, 4637-4646, 1989
Ma Be	Query Match 9.2%; Score 121.5; DB 1; Length 590; Best Local Similarity 25.5%; Pred. No. 0.86; Matches 64; Conservative 24; Mismatches 124; Indels 39; Gaps 9;	A;Title: DNA nucleotide sequence analysis of the immediate-early gene of pseudorables A;Reference number: S04713; MUID:89315207; PMID:2546124 A;Accession: S04713
Qy Dp	28 PPPALCARFVKEPRGLSAASPPLAETGAPRRFRRSVPRGEAAGAVQELARALAHLLE 84	A; Molecule type: DNA A; Residues: 1-1460 <che> C; Superfamily: herpesvirus immediate-early protein IE175 C; Keywords: DNA binding; early protein; transcription regulation</che>
Qy Dp	85 AERQERARAEAQEAEDQQARVLAQLLRVWGAPRNSDPALGLDDDPDAPAAQLARA 139 ,	Query Match 9.1%; Score 119.5; DB 1; Length 1460; Best Local Similarity 25.2%; Pred. No. 2.9; Matches 75; Conservative 24; Mismatches 110; Indels 89; Gaps 14;
& g	140 LLRARLDPAALAAQLVPAAALRPRPPVYDDGPAGPDAEEAGDETPDVD 191 :	OY 3 GSPLLWGPRAGGVGLLVLLLGLFRPPPALCARPVKEPRGLSAASPPLAETGAPRFFR 60
oy g	192 PELLRYLLGRILAGSADSEGVAAPRRLRRAADHDVGSELPPEGVLGALLRVKRLETP 248  1	Oy 61 RSVPRGEAAGAVQELARALAHLLEAERQERARAEAQEA-EDQQARVLAQLLRVWGAPRNS 119 1

A; Reference number: A45344; MUID:91021039; PMID:2171211 A; Accession: A4534 A; Status: translation not shown A; Status: translation not shown A; Molecule type: DNA A; Residues: 1.1446 < VUC> A; Cross references: GB: M34651; NID:g334070; PIDN:AAA47470.1; PID:g334071 C; Superfamily: herpesvirus immediate-early protein IE175 C; Keywords: DNA binding; early protein; transcription regulation Query Match Best Local Similarity 26.6%; Pred. No. 3.6; Batches 83; Conservative 22; Mismatches 97; Indels 110; Gaps 15;	OY 16 GLLVLLLGIFRPPPALCARPVKEPRGLSAASPPIAE-TGAPRRFRSVPRGEA 68	:      :	Query Match       8.9%; Score 117; DB 1; Length 643;         Best Local Similarity 22.2%; Pred. No. 1.8;       1.8;         Matches 66; Conservative 40; Mismatches 101; Indels 90; Gaps 14;         Qy 8 WGPRAGGVGLUVLLLGLERPPPALCARPVKEPRGLSAASPPLAETGAPRRFRRSVPR 65   1
Qy   120   DPALGLDDDPDAPAAQLARALLRARLDPAALAAQLVPAPVPAAALRPRPP 169	EESULT 12 EDBE75 immediate early protein IE175 - human herpesvirus 1 C; Species: human herpesvirus immediate-early protein IE175 C; Supering 1 C; Species: human herpesvirus immediate-early protein IE175 C; Supering 1 C;	Query Match         9.0%; Score 118.5; DB 1; Length 1298;           Best Local Similarity 24.9%; Pred. No. 3;         Matches 88; Conservative 24; Mismatches 121; Indels 121; Gaps 15;           Qy         2 AGSP-LLWGPRAGGVGLLVLLIGIERRPPALCARPVKEPR	Oy 203 -LAGSADSECVAAPRRIRRAADHDVGSELPPEGVLG-ALLRVKRLETPAPCVPA 254

145 GQICAQVIDLVDMQDAQIRGLERRIQDRLGLRDNLPVAGIQAPPSSPIGQ------ 194

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10;
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A,Residues: 1-1677 <WAN>
A;Cross-references: EMBL:AF051945; NID:92970645; PID:92970646; PIDN:AAC06023.1
A;Experimental source: cardiac muscle; stage early embryo
                                                                                                                                                                                                                                                   Xin protein, stage early embryo - mouse
C;Species: Mus musculus (house mouse)
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
C;Accession: T14267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1053 LQEAMQNLRLATAEAQSLHQQ---VLSR-----HPQGSDPVATSMPVQDVLQASTPATG 1103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   195 ------PIASSSLQPIP----GSSSSPADLDGIWTPRQIDPRLSRVAXNPFLP 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            82 LLEAERQER-ARAEAGEAEDQQARVLAQLLRVWGAPRNSDP-ALGLDDDPDAPAAQLARA 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     140 LLRARLDPAALAAQLVPAPVPAAALRPRPPVYDDGPAGPDAEEAGDETPDVDPELLRYLL 199
146 DPAALAAQLVPAPVPAAALRPRPPVYDDGPAGPDAEEAGDETP-DVDPELLRYLLGRILA 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             200 GRILAGSADSEGVAAPRRLRRAADHDVGSELPPEGVLGALLRVKRLETPAPQVPAR--RL 257
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                                                                                                                      205 GSADSEGVAAPRRLRRAADHDVGSELP--PEGVLGALLR-VKRLETPAPQ-VPARRL 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            41;
                                                                                                                                                                                                                                                                                                                                        R;Wang, D.Z.; Lin, J.J.C.
submitted to the EMBL Data Library, March 1998
A;Bescription: Involvement of a novel gene, Xin, in cardiac looping.
A;Reference number: 217948
A;Accession: T14267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 8.8%; Score 116.5; DB 2; Length 1677; Best Local Similarity 25.9%; Pred. No. 5.2; Matches 63; Conservative 26; Mismatches 113; Indels 41;
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GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

April 4, 2003, 14:09:29; Search time 11 Seconds (without alignments) 980.350 Million cell updates/sec Run on:

ritle:
Perfect score:
Sequence:

US-09-803-589-6 1319 1 MAGSPLLWGPRAGGVGLLVL......RVKRLETPAPQVPARRLLPP 260

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

Total number of hits satisfying chosen parameters: 112892 segs, 41476328 residues Searched:

112892

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt\_40:\* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Description	O13164 homo sapien	rhodo	P11675 pseudorable	P08392 herpes simp	P33479 pseudorabie			P50548 homo sapien	mus	Q9wvs8 mus musculu	P06401 homo sapien		rattn	homo	homo	homo		P29836 bovine herp	_	h nuc	homo	homo	homo	drosc	P09790 neisseria g	xenobns	P17437 xenopus lae	Q9npg4 homo sapien	mus	Q91zi0 mus musculu		-	P41110 oryctolagus
SUMMAKIES	MK07_HUMAN	SBCC_RHOCA	IE18_PRVIF	ICP4_HSV11	IE18_PRVKA	GAG_SFV3L	VGF_HUMAN	ERF_HUMAN	ERF_MOUSE	MK07_MOUSE	PRGR_HUMAN	TEGU_HSV11	NEB2_RAT	BAT2_HUMAN	TCOF_HUMAN	SPCQ_HUMAN	FXE3_HUMAN	ICPO_HSVBK	M3KA_HUMAN	NCR2_HUMAN	TIZ2_HUMAN		3BP1_HUMAN	MOF_DROME	IGA_NEIGO	YB56_XENLA	XP2_XENLA	PC12_HUMAN	NMBL_MOUSE	CLR3_MOUSE	ODO2_MYCTU		IF4G_KABIT
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Length	815	1238	1461	1298	1446	643	919	248	551	908	933	3164	817	2142	1411	2564	319	929	954	2517	395	703	622	827	1532	336	439	1184	603	3301	553	628	1402
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Score	124.5	123	119.5	118.5	118	117	116.5	116	_	113.5		113.5	112	111	110	109.5	108	107	107	107	106.5	106	102	105	105	103.5	103.5	103.5	103	103	102.5	102.5	102.5
Result No.	-	8	e	4	S	9	7	œ	on :	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	29	30	31	32	33

34         102.5         7.8         3530         1         MY15_HUMAN           35         102         7.7         825         1         CPO_HSV2H           37         101.5         7.7         57         1         BAG3_MOUSE           38         101.5         7.7         1395         1         IFAG_HUMAN           39         101         7.7         450         1         CYL_PARDE           40         101         7.7         633         1         PAD_HUMAN           41         101         7.7         676         1         CCAB_LHOMAN           42         101         7.7         676         1         CCAB_LHOMAN           43         100.5         7.6         642         1         DP3X_SALTY           40         7.6         1729         1         TABP_HUMAN			0911v1 mus musculu									Q9c0c2 homo sapien
102.5 7.8 102.5 7.7 101.5 7.7 101.5 7.7 101 7.7 101 7.7 101 7.7 101 7.7 100.5 7.6	MY15_HUMAN	ICPO_HSV2H	BAG3_MOUSE	IF4G_HUMAN	TTP_HUMAN	CY1_PARDE	MIS_BOVIN	PAN2_HUMAN	ICP0_HSVBJ	CCAB_RABIT	DP3X_SALTY	TABP_HUMAN
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## ALIGNMENTS

RESULT MK07_H	1 dman
£	MKO7_HUMAN STANDARD; PRT; 815 AA.
A C	QU31164; Q16634;
5 5	OI-NOV-1997 (Rel 35, Tagt seminance undate)
5 5	16-07T-2001 (Rel 40. Last annotation indate)
DE	Mitogen-activated protein kinase 7 (EC 27.1) (Extracellular signal-
DE	K4) (BMK1 kinase).
S	MAPK7 OR PRKM7 OR ERK5 OR ERK4.
SO	).
3 8	Manualia, Enthorats, Confracts, Cranlata; Vertebrata; Euteleostomi;
3 8	Manualia; Authetia; Filmates; Catarinini; Hominiaae; Homo. Nobi mayin-9606.
R S	
RP	SEQUENCE FROM N.A.
Z,	TISSUE=Fetal brain;
RX	MEDLINE-95279403; PubMed-7759517;
RA	Zhou G., Bao Z.Q., Dixon J.E.;
RI	"Components of a new human protein kinase signal transduction
RT	pathway.";
2 2	J. BIOL. Chem. Z/O:12003-12009(1993).
Z C	מיא אוכום מיאמונים
¥ 5	SECURICE FROM N.A.
2 2	TINDUCE FIGURE OF THE STATE OF
X E	MEDILINE-WORLD 403-049, PUDMEQH-VORDOZEN, PUDMEQH-VORDOZEN,
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1 10	Filmary Sciucture of Bown: 313.315.234.1006.
3 5	DIOCHENI DIOPNYS. RES. COMMUN. 213:113-744(1932). -!- FINGTION: MEKS AND ERKS INTERBACTETING. WITH ONE ANOTHER AND
3 5	NOT WITH MERITERAL OR MERZYERS DATHWAYS
) 	ENZYME REGILATION: ACTIVATED BY TYROSINE AND THREONINE
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ပ္ပ	-i- TISSUE SPECIFICITY: EXPRESSED IN MANY ADULT TISSUES. ABUNDANT IN
႘	HEART, PLACENTA, LUNG, KIDNEY AND SKELETAL MUSCLE. NOT DETECTABLE
ပ္ပ	IN LIVER.
ខ	-!- DOMAIN; THE SECOND PROLINE-RICH REGION MAY INTERACT WITH ACTIN
ဗ္ဗ	TARGETING THE KINASE TO A SPECIFIC LOCATION IN THE CELL.
ဗွ	PTM: AUTOPHOSPHORYLATED ON THREONINE AND TYROSINE RESIDUES, WHEN
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DR	029725;
DR	U29726;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11;
                                                                                                                                                                        PROSITE; PS01351; MAPK; 1.
PROSITE; PS01351; MAPK; 1.
PROSITE; PS0107; PROTEIN KINASE_ATP; 1.
PROSITE; PS0010B; PROTEIN_KINASE_DOM; 1.
PROSITE; PS0010B; PROTEIN_KINASE_ST; 1.
Transferase; Serine/threonine-protein kinase; ATP-binding; Cell cycle;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     419 PSPWAPSGD------CAMESPPPAPPCPGPAPDTIDLILQPPPPVSEPAPPKKDGA 469
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             63 VPRGEAAGAVQELARALAHLL--------EAERQERARAEAQEAED 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     470 ISDNTKAALKAALLKSLRSRLRDGPSAPLEAPEPRKPVTAQERQREREEKRRRQERAKE 529
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           101 QQARVLAQLLRVWGAPR----NSDPALGL---DDDPDAPAAQLARALLRARLDPAALAAQ 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  154 LVPAPVPAAALRPRPPVYDDGPAGPDAEEAGDETPDVDPELLRYLLGRILAGSADSEGVA 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          81; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5 PLLWGPRAGGVGLLVLLLLGLFRPPPA--LCARPVKEPRGLSAASPPLAETGAPRRFRRS 62
                                                                                                                                                                                                                                                                                                                                                                                                      ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
BY SIMILARITY.
PHOSPHORYLATION (ACTIVATES THE KINASE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PHOSPHORYLATION (ACTIVATES THE KINASE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AREGRIRPHRCLCS -> GPVKVEPAHTAASVA (IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SVPAPAPAPAPTPTPVQPTSPPPGPLAQPTGPQ-----PQSAGSTSGPVPQPACPPPG--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         214 APRILRRAADHDVGSELPPEGVLGALLRVKRLETPAPQ------VPARRLLPP 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rhodobacter capsulatus (Rhodopseudomonas capsulata).
Bacteria; Proteobacteria; alpha subdivision; Rhodobacter group;
Rhodobacter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 1; Length 815;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; Score 124.5; DB 1; Length 81; Pred. No. 0.51; 31; Mismatches 116; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -> V (IN REF. 2).
379AD69803207CCF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Nuclease sbccD subunit C.
                                                                                                                                                                                                                                                                                                        PROTEIN KINASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SIMILARITY
                                                                                                                                                                                                                                                                                                                                              PRO-RICH 1.
                                                                                                                                                                                                                                                                                                                                                                 POLY-ARG.
PRO-RICH 2.
                                                                                                                                                                                                                                                                                                                           POLY-ALA.
                                                                     InterPro; IPR003527; MAP_kin.
InterPro; IPR003529; MAP_kin.
Pfam; PF00069; pkinase; 1.
ProDom; PD000001; Euk_pkinase; 1.
SMART; SM00220; S_TKC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REF. 2)
L -> V
                                                        InterPro; IPR000719; Euk_pkinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (BY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          88636 MW;
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STRAIN-SB1003 / St Louis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
24941; 1HCL.
HGNC:6880; MAPK7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            815 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=1061;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 19
                                                                                                                                                                                                                                                                                     Phosphorylation
                                       MIM; 602521; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SBCC_RHOCA
068032;
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BINDING
ACT_SITE
MOD_RES
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    64 PRGEAAGAVQELARALAHLLEAERQE------RARAEAQEAEDQQARVLAQLL 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    904
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     690 WGDTQPRVSA------APLAPALPGTP--DPTALAAAQDRLC------AL 725
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   905 AAQRAQQAAAAD-----LATAQAALAAAEARAA--ETARAASEAATAQRAAEADLAAA 955
                                                       Proc. Natl. Acad. Sci. U.S.A. 94:9384-9388(1997).

Proc. Natl. Acad. Sci. U.S.A. 94:9384-9388(1997).

-!- FUNCTION: SbcCD cleaves DNA hairpin structures. These structures can inhibit DNA replication and are intermediates in certain DNA recombination reactions. The complex acts as a 3'->5' double strand exonuclease that can open hairpins. It also has a 5' single-strand endonuclease activity (By similarity).
-!- SUBUNIT: Heterodiane of sbcC and sbcD (By similarity).
-!- SIMILARITY: BELONGS TO THE SMC FAMILY. SBCC SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
Vicek C., Paces V., Maltsev N., Paces J., Haselkorn R., Fonstein M.; "Sequence of a 189-kb segment of the chromosome of Rhodobacter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R EMBL; AF010496; AAC16118.1;
R InterPro; IPR003439; ABC_transportr.
Hydrolase; Wuclease; Exonuclease; Endonuclease; DNA replication;
W Hydrolase; Wuclease; Exonuclease; Endonuclease; DNA replication;
W DNA recombination; ATP-binding; Coiled Coil.
T NP_BIND 37 44 ATP (POTENTIAL).
T DOMAIN 395 438 COILED COIL (POTENTIAL).
FT DOMAIN 521 600 COILED COIL (POTENTIAL).
FT DOMAIN 724 770 COILED COIL (POTENTIAL).
FT DOMAIN 901 943 COILED COIL (POTENTIAL).
FT DOMAIN 1019 1052 COILED COIL (POTENTIAL).
FT DOMAIN 1019 1052 COILED COIL (POTENTIAL).
FT DOMAIN 22666C633859AE1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8 WG---PRAGGVGLLVLLLLGLFRP-PPALCARPVKEPRGLSAASPPLAETGAPRRFRRSV 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      111 RVWGAPRNSDPALGL------DDDPDAP--------AAO-----L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             785 RTEAAARRDGLALALAPALARAGEDDPAAPGLAERLAATVSAVGAARTGLQAAQEALSAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; Score 123; DB 1; Length 1238;
; Pred. No. 0.95;
18; Mismatches 114; Indels 104;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pseudorabies virus (strain Indiana-Funkhauser / Becker) (PRV).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ARALLRARLDPAALAAQLVPAPVPA-----AALR-PRPPVYDDGPAGPD----
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01-APR-1990 (Rel. 14, Last sequence update)
01-FEB-1994 (Rel. 28, Last annotation update)
Immediate-early protein IE180.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1461 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LEAAAMS -- AAELAALIALPP 974
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      26.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
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GENES.
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                                                                                                                                                                                                                                                                                                                                                                                                 between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on it use by non-profit institutions as long as its content is in no we modified and this statement is not removed. Usage by and for commercia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AGAVQELARALAHLLEAERQERARAEAQEAEDQQARVL-----AQLLRVWGAPRNSD 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121 PALGLDD-DPDAPAAQLARALLRARLDPAALAAQLVPAPVPAAALRPRPPVYDDGPAGPD 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               817 PAPGLPPLWPEQPGL--------VVPAPAAAGAP-SGLPGSGPSSPA 856
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IGRILAGSA----DSEGVAAPRRLRRAADHDVGSELPPEGVLGALL-----RVKRLET 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    917 SGSALRGDGHGHRDDEEDRGPRRKRRSLGLGPAPDPAPALVSSSSSSSSSEDDRLRRPLG 976
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GLLVLLLLGLFRPPPALCARPVKEPRGLSAASPPLAE-TGAPRRFRRSVP-----RGEA 68
                                                                                                                                                                                                                      Submitted (NOV-1989) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: THIS IE PROTEIN IS A MULTIFUNCTIONAL PROTEIN CAPABLE OF MIGRAFING TO THE NUCLEUS, BINDING TO DNA, TRANS-ACTIVATING OTHER VIRAL GENES, AND AUTOREGULATING ITS OWN SYNTHESIS.
-!- SUBCELLULAR LOCATION: NUCLEUS OF INFECTED CELLS.
-!- PTM: A LONG STREFCH OF SERINE RESIDUES MAY BE A MAJOR SITE OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                857 STKSGSSTKSSSGTKSGLSGSSGYASSPAAGPDPAPERRKKKRRAPGARRPGDGEEDEGL
                                                                                                                       "DNA nucleotide sequence analysis of the immediate-early gene of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 1461;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF03584; Herpes_ICP4_N; 1.—
Pfam; PF03585; Herpes_ICP4_C; 1.
Early protein; Transcription regulation; Trans-acting factor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       27; Mismatches 105; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7F31E7ABE403B208 CRC64;
                                                                                                                                                                                                                                                                                                                                                   SIMILARITY: BELONGS TO THE ICP4/IE140/IE180 FAMILY.
Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
Alphaherpesvirinae; Varicellovirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNA-binding; Phosphorylation; Nuclear protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9.1%; Score 119.5; I
                                                                                                                                       pseudorabies virus.";
Nucleic Acids Res. 17:4637-4646(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  POLY-SER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DIR; S04713; EDBEIF.
InterPro; IPR005205; Herpes_ICP4_C.
InterPro; IPR005206; Herpes_ICP4_N.
                                                                                      MEDLINE-89315207; PubMed-2546124;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1461 AA; 149833 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; X15120; CAA33214.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity 25.18;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                996
                                                                                                                                                                                                                                                                                                                                 PHOSPHORYLATION
                                                                  SEQUENCE FROM N.A.
                                    NCBI_TaxID=31523;
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PMPEHPA 983
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                                                                                                                                                                                                             Cheung A.K.;
                                                                                                        Cheung A.K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        77;
                                                                                                                                                                                             REVISIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local S
Matches 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
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ICP4\_HSV11

RESULT 4

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                                                                                                                                                                                                                                                                                     of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ICP4 ALSO ACTS AS A TRANSCRIPTIONAL ACTIVATOR OF BETA AND GAMMA GENES. ICP4 BINDS WITH HIGH AFFINITY TO THE SEQUENCE 5'-ATGGTC-3'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENES. ICP4 BINDS WITH HIGH AFFINITY TO THE SEQUENCE 5'-ATCGTC-5'-1-SUBUNIT: HOMODIMER.

-1-SUBCELLULAR LOCATION: NUCLEUS OF INFECTED CELLS.

-1-PTM: IC4 IS ADP-RIBGSYLATED.

-1-PTM: THE LONG STRETCH OF SER IS A MAJOR SITE OF PHOSPHORYLATION.

ONLY THE PHOSPHORYLATED FORMS OF ICP4 ARE CAPABLE OF INTERACTING.
                           01-AGG-1988 (Rel. 08, Created)
01-AGG-1988 (Rel. 08, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
Trans-acting transcriptional protein ICP4 (Transcriptional activator
                                                                                                                                                                                                                              MEDLINE-88274377; PubMed=2839594; McGeoch D.J., Dalrymple M.A., Davison A.J., Dolan A., Frame M.C., McNab D., Perry L.J., Scott J.E., Taylor P.; The complete DNA sequence of the long unique region in the genome
                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
MEDLINE-86148504; PubMed-3005980;
McGeoch D.J., Dolan A., Donald S., Brauer D.H.K.;
"Complete DNA sequence of the short repeat region in the genome of
                                                                                                                                                                                                                                                                                                                                                                                                                                                  [3]
MEDLINE-90174974; PubMed=2155403;
Wu C.-L., Wilcox K.W.;
"Codons 262 to 490 from the herpes simplex virus ICP4 gene are sufficient to encode a sequence-specific DNA binding protein.";
Nucleic Acids Res. 18:531-538(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WITH BETA OR GAMMA GENES.
SIMILARITY: BELONGS TO THE ICP4/IE140/IE180 FAMILY.
                                                                                                                                 Herpes simplex virus (type 1 / strain 17).
Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
Alphaherpesvirinae; Simplexvirus.
PRT; 1298 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFLUENCE OF PHOSPHORYLATION ON FUNCTION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                  herpes simplex virus type 1.";
Nucleic Acids Res. 14:1727-1745(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PIR; A23510; EDBE75.
INTERPRO; IPR005205; Herpes_ICP4_C.
INTERPRO; IPR005206; Herpes_ICP4_N.
Pfam; PF03584; Herpes_ICP4_N; 1.
                                                                                                                                                                                                                                                                                                                   Gen. Virol. 69:1531-1574(1988)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; L00036; AAA96675.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; L00036; AAA96688.1; --
EMBL; X14112; CAA32286.1; --
EMBL; X14112; CAA32278.1; --
EMBL; X06461; CAA29763.1; --
                                                                                                                                                                                                                                                                                                       type 1
                                                                                                  IE175) (Alpha-4 protein).
ICP4 OR IE175 OR RS1.
STANDARD;
                                                                                                                                                                                                                                                                                                   herpes simplex virus
                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                 NCBI_TaxID=10299;
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129
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GAG_SFV3L
     DR WE BOR SOR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 646
                                                                                                                                                                                                             355 SGAPAAVWAPELGDAAQQYALITRLLYTPDAEAMGWLQNPRVVPGDVALDQACFRISGAA 414
                                                                                                                                                                                                                                                                                                                                                                              117 RNSDPALGLDDDPDAP-----AAQLAR----ALLRARLDPAALAAQLVPAPV 159
                                                                                                                                                                                                                                                                                415 RNSSSFITGSVARAVPHLGYAMAAGRFGWGLAHAAAAVAMSRRYDRAQKGFLLTSLRRAY 474
                                                                                                                                                                                                                                                                                                              AHLLEAER-------QERARAEAQEAEDQQ------ARVLAQLLRVWGAP 116
                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                   79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-91021039; PubMed-2171211;
Vicek C., Kozmik Z., Paces V., Schirm S., Schwyzer M.;
"Pseudorabies virus immediate-early gene overlaps with an oppositely oriented open reading frame: characterization of their promoter and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        enhancer regions.";
Virology 179:365-377(1990).
-!- FUNCTION: THIS IE PROTEIN IS A MULTIFUNCTIONAL PROTEIN CAPABLE
OF MIGRATING TO THE NUCLEUS, BINDING TO DNA, TRANS-ACTIVATING
OTHER VIRAL GENES, AND AUTOREGULATING ITS OWN SYNTHESIS.
-!- SUBCELLULAR LOCATION: NUCLEUS OF INFECTED CELLS.
-!- PTM: A LONG STRETCH OF SERINE RESIDUES MAY BE A MAJOR SITE OF
                                                                                                                                                                                                                                                                                                                                                                                                  -----GLSAASPPLAETGAPRRFRRSVPRGEAAGAVQ--------ELARAL
                                                                                                                                                                                                                                                                                                                                               475 APLLARENAALTGAAGSPGAGADDEGVAAVAAAAPGERAVPAGYGAAGILAALGRLSAAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              591 PGLAGARPASPPRPEGPAGP----ASPPPPHADAPRLRAWLRELREVRDALVLARLRGDL
   regulation; Trans-acting factor;
; Nuclear protein; ADF-ribosylation.
SER-RICH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            203 -LAGSADSEGVAAPRRLRRAADHDVGSELPPEGVLG-ALLRVKRLETPAPQVPA 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels 121;
                                                                                                                Length 1298;
                                                                                                                                                                                  2 AGSP-LLWGPRAGGVGLLVLLLGLFRPPPALCARPVKEPR------
                                                                                1298 AA; 132843 MW; 4F32E04C95CA9344 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PHOSPHORYLATION.
-1- SIMILARITY: BELONGS TO THE ICP4/IE140/IE180 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pseudorables virus (strain Kaplan) (PRV).
Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
Alphaherpesvirinae; Varicellovirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                               PA-AALRPRPPVYDDGPAGPDAEEAGDETPDVDPELLRYLLGRI---
                                                                                                             ch 9.0%; Score 118.5; DB 1;
1 Similarity 24.9%; Pred. No. 1.9;
88; Conservative 24; Mismatches 121;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Last sequence update)
Last annotation update)
Pfam; PF03585; Herpes_ICP4_C; 1.
Early protein; Transcription regulation;
DNA-binding; Phosphorylation; Nuclear prc
DOMA.N. 176 199 SER-RICH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-FEB-1994 (Rel. 28, Created)
01-FEB-1994 (Rel. 28, Last seq
01-FEB-1994 (Rel. 28, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Immediate-early protein IE180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
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P33479;
                                                 DOMAIN
DNA_BIND
SEQUENCE
                                                                                                             Query Match
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                            696 GVLERLL-----PCPLRLPAPARAPAALGPAC--LEEVTAALLALRDAIPGAGPAERROA 748
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        69 AGAVQELARALAHLLEAERQERARAEAQEAEDQQARVLAQLLRVWGAPRNSDPALGLDDD 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PDAPAAQLARALLRARLDPAALAAQL------VPAPVPAAALRPRPVYDDGPAG 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    197
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                                                                                                                                                                                                                                                                                                                                   97; Indels 110; Gaps
                                                                                                                                                                                                                                                                                                                                                                             16 GLLVLLLLGLFRPPPALCARPVKEPRGLSAASPPLAE-TGAPRRFRRSVP-----RGEA 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Virology 186:597-608(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    --VAAARLAEA--AARPGPAEPAPGLPPLWPEQPGLVVPAPAPAAAGAP-SGLPGSGPSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            844 PASTKSSSSTKSSSSTKSGLSGSSGYASSPAAGPDPAPERRKKRRAPGARRPGDGEEDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           198 -LLGRILAGSA----DSEGVAAPRRLRRAADHDVGSELPPEGVLGALL-----RV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Genomic organization and expression of simian foamy virus type 3 ({\rm SFV}\!-\!3) ",
                                                        InterPro; IPR00520b; helpe__CP4_N; 1.
Pfam; PF03584; Herpes_ICP4_C; 1.
Pfam; PF03585; Herpes_ICP4_C; 1.
Barly protein; Transcription regulation; Trans-acting factor; DNA-binding; Phosphorylation; Nuclear protein.
DNA-binding; Phosphorylation; PolY-SER.
DNA-binding; Phosphorylation; PolY-SER.
                                                                                                                                                                                                                                                                                  Query Match 8.9%; Score 118; DB 1; Length 1446; Best Local Similarity 26.6%; Pred. No. 2.3; Matches 83; Conservative 22; Mismatches 97; Indels 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-92124734; Pubmed-1310187;
Renne R., Friedl E., Schweizer M., Fleps U., Turek R.,
Neumann-Haefelin D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-AUG-1992 (Rel. 23, Last sequence update)
01-JUL-1993 (Rel. 26, Last annotation update)
03-JUL-1993 (Rel. 26, Last annotation update)
04-GAG.
Simian foamy virus (type 3 / strain LK3) (SFV-3).
Viruses; Retroid viruses; Retroviridae; Spumavirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           643 AA.
                 PIR; A45344; A45344.
InterPro; IPR005205; Herpes_ICP4_C.
InterPro; IPR005206; Herpes_ICP4_N.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-AUG-1992 (Rel. 23, Created)
01-AUG-1992 (Rel. 23, Last seq
01-JUL-1993 (Rel. 26, Last ann
M34651; AAA47470.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  959 RRPLGPMPEHPA 970
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67286 MW; CD1920610201BEB9 CRC64;

616 AA;

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SEQUENCE
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                                                                                 14;
                                                                                                                                                                                                103 ARVLAQLL------RVWGAPRNSDPALGLDDD------PDAPAAQLARALLRARL 145
                                                                                                                                                    145 GOICAQVIDLVDMQDAQIRGLERRIQDRLGLRDNLPVAGIQAPPSSPIGQ----- 194
                                                                                                                                                                                                                                             146 DPAALAAQLVPAAPVPAAALRPRPPVYDDGPAGPDAEEAGDETP-DVDPELLRYLLGRILA 204
                                                                                                                                                                                                                                                               -----PIASSSLQPIP-----GSSSSPADLDGIWTPRQIDPRLSRVAYNPFLP 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               chromosomal assignment
                                                                                  Gaps
                                                                                                      8 WGPRAGGVGLLVLLLLGLFRPPPALCARPVKEPRGLSAASP--PLAETGAPRRFRRSVPR 65
                                                                                                                                                                                                                                                                                                       205 GSADSEGVAAPRRLRRAADHDVGSELP--PEGVLGALLR-VKRLETPAPQ-VPARRL 257
                                                                                                                    -1- FUNCTION: MAY BE INVOLVED IN THE REGULATION OF CELL-CELL INTERACTIONS OR IN SYNATOGENESIS DURING THE MATURATION OF THE NERVOUS SYSTEM (By similarity).

1- SUBCELLULAR LOCATION: Stored in secretory vesicles and then secreted (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                 90;
                                                          Length 643;
                                                                                 40; Mismatches 101; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NEUROSECRETORY PROTEIN VGF. ASP/GLU-RICH (ACIDIC).
                                 C53A0575BA9B5949 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Canu N., Possenti R., Ricco A.S., Rocchi M., Levi A., "Cloning, structural organization analysis and chromo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          of the human gene for neurosecretory protein VGF.";
Genomics 45:443-446(1997).
                                                          DB 1;
                                                                                                                                                                                                                                                                                                                                                                                             15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Neurosecretory protein VGF precursor.
                                                                                                                                                                                                                                                                                                                                                                            Ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -1- TISSUE SPECIFICITY: Expressed in brain.
                                                        8.9%; Score 117; 22.2%; Pred. No. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE=Placenta;
MEDLINE=98008940; PubMed=9344675;
InterPro; IPR004957; Spuma_gag. Pfam; PF03276; Gag_spuma; 1. Core protein; Polyprotein.
                                   69785 MW;
                                                                                                                                                   66 GEAAGAVQELARALAHL-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; Y12661; CAA73210.1; -. Genew; HGNC:12684; VGF.
MIM; 602186; -.
                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         22
616
447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Growth factor; Signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                       sapiens (Human)
                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                   643 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=9606;
                                                                              99
                                                                                                                                                                                                                                                                                                                                                                         VGF_HUMAN
015240;
                                   SEQUENCE
                                                          Query Match
                                                                       Local
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MEDLINE-96030784; PubMed-7588608;
Sgouras D.N., Athanasiou M.A., Beal G.J. Jr., Fisher R.J., Blair D.G.,
Mavrothalassitis G.J.;
                                                                                                                                                                                                                                                                                                                                                                         128 DPDAPAAQLARALLRARLDPAALAAQLVPAPVPAAALRPRPPVYDDGPAGPDAEEAGDET 187
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                                                                                                    61; Gaps
                                                                                                                                                                         11 RAGGVGLLVLLLL-GLFRPPPALCARPVKEPRGLSAA-SPPLAETGAPRRFRRSVPRGEA 68
                                                                                                                                                                                                                   IN CELLULAR PROLIFERATION.
-!- SUBCELLULAR LOCATION: Nuclear.
-!- PTM: PHOSPHORYLATED BY MULTIPLE KINASES INCLUDING PROBABLY ERK2.
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Lamerdin J.E., McCready P.M., Skowronski E., Viswanathan V.,
Burkhart-Schultz K., Gordon L., Dias J., Ramirez M., Stilwagen S.,
Phan H., Velasco W., Do L., Regala W., Terry A., Garnes J.,
Danganan L., Erler A., Christensen M., Georgescu A., Avila J., Liu S
Attix C., Andreise T., Trankheim M., Amico-Keller G., Coefield J.,
Duartre S., Lucas S., Bruce R., Thomas P., Quan G., Kronniller B.,
Arellano A., Sanders C., Ow D., Nolan M., Trong S., Kobayashi A.,
Olsen A.S., Carrano A.V.;
"Sequence analysis of a 3.2 Mb region in 19q13.2 between CYP2FI and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (FEB-1999) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: POTENT TRANSCRIPTIONAL REPRESSOR THAT BINDS TO THE H1
ELEMENT OF THE ETS2 PROMOTER. MAY REGULATE OTHER GENES INVOLVED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
ETS-domain transcription factor ERF (Ets2 repressor factor).
                              Length
                                                                                                    Indels
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                                                                                                27; Mismatches 109;
                       8.8%; Score 116.5; D
25.9%; Pred. No. 1.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        548 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            200 PGPERVWRASWGEFOARVPERAPLPP 225
Query Match
Best Local Similarity 25.9%;
....has 69; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens (Human)
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P50548; Q9UPI7;
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MEDLINE-97282708; PubMed-9136988;
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Best Local S
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MOD_RES
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  use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12;
non-profit institutions as long as its content is in no
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   179 DAEEAGDETPDVDPELLRYLLGRILAGSADSEGV----AAPRRLRRAADHDVGSELPPEG 234
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        246 S----PFPVSPLAGPGSLLPPQLSPA-----LPMTPTHLAYTPSPTLSPMYPSGGGGP 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             26 FRPPPALCAR---PVKEPRGLSAASPPLAETGAPRRFRRSVPRGEAAGAVQELARALAHL 82
                                                                                                                                                                                 InterPro; InterP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBL_raxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A PHOSPHORYLATION SITE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          86;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8.8%; Score 116; DB 1; Length 548; 24.1%; Pred. No. 1.2; ative 24; Mismatches 92; Indels
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PHOSPHORYLATION (BY MAPK1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C93A155394B1EEDD CRC64;
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R -> P (IN REF. 2)
A -> G (IN REF. 2)
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                                                                                                                                                                                                                                                                                                                                                                                                                 POLY-SER.
POLY-GLY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      POLY-SER.
POLY-PRO.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              58776 MW;
                                                                                           EMBL; U15655; AAA86686.1; -.
EMBL; AC006486; AAD11987.1;
HSSP; Q01543; 1FLI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        64; Conservative
                                                                                                                                                      TRANSFAC; T04885; -. Genew; HGNC:3444; ERF.
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MUTAGEN
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REMEL; U58533; AAC09474.1; -.
REMEL; U58534; AAC09474.1; -.
REMEL; U58534; ACC09474.1; -.
REMEL; U58534; IFLI.
REMEL; U59637; IFLI.
REPPROJ. IPRO00418; Ets.
REPROJ. PF00178; Ets.
REPROM54; ETS.
REPROM54; ETS.
REPROM571E; PS00346; ETS.
REPROSITE; PS00346; ETS.
REPROS
Liu D., Paviopoulos E., Modi W., Moschonas N., Mavrothalassitis G.J.;
"ERF: genomic organization, chromosomal localization and promoter
analysis of the human and mouse genes.";
Oncogene 14:1445-1451(1997).
-I- FUNCTION: POTENT TRANSCRIPTIONAL REPRESSOR THAT BINDS TO THE HI
ELEMENT OF THE ETS2 PROMOTER. MAY REGULATE OTHER GENES INVOLVED
IN CELLULAR LOCATION: Nuclear.
-I- SUBCELLULAR LOCATION: Nuclear.
-I- PTM: PHOSPHORYLATED BY MULTIPLE KINASES INCLUDING PROBABLY ERKZ.
PHOSPHORYLATED REGISTER THE ACTIVITY OF ERF (BY SIMILARITY).
-I- SIMILARITY: BELONGS TO THE ETS FAMILY.
                 Mavrothalassitis G.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           294
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POLY-PRO.
PHOSPHARITY) (BY MAPK1) (BY SIMILARITY).
5AC1B72FB2743FE5 CRC64;
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POLY-GLY.
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Q9WVS8;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   --- FUNCTION: MEKS AND ERKS INVERACT SPECIFICALLY WITH ONE ANOTHER AND NOT WITH MEKL/ERK1 OR MEKZ/ERK2 PATHAAYS (BY SIMILARITY).
--- ENZYME REGULATION: ACTIVATED BY TYROSINE AND THREONINE PHOSPHORYLATION (BY SIMILARITY).
--- DOMAIN: THE SECOND PROLINE-RICH REGION MAY INTERACT WITH ACTIN
                                                                                                                                                                                                                                                                                                                                               Kamakura S., Moriguchi T., Nishida E.;
"Activation of the protein kinase ERK5/BMK1 by receptor tyrosine
kinases: identification and characterization of a signaling pathway to
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Mitogen-activated protein kinase 7 (EC 2.7.1.-) (Extracellular signal-regulated kinase 5) (ERK-5) (BMK1 kinase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATP-binding; Cell cycle;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TARGETING THE KINASE TO A SPECIFIC LOCATION IN THE CELL.
THE C-TERMINAL PART OF THE KINASE, WHICH COULD HAVE A REGULATORY
ROLE, IS ABSENT (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (BY SIMILARITY). PHOSPHORYLATION (ACTIVATES THE KINASE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PHOSPHORYLATION (ACTIVATES THE KINASE)
                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ROLE, IS ABSENT (BY SIMILARITY).
SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
MAP KINASE SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8.6%; Score 113.5; DB 1; Length 806; 22.8%; Pred. No. 2.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (OCT-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          E7CC41C4BBDE0633 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
Transferase; Serine/threonine-protein kinase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROTEIN KINASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; ABULSSIC.,
HSSP; P24941; 1HCL.
HGCD; MGCD; MGIT346347; Mapk7.
InterPro; IPR000719; Euk pkinase.
InterPro; IPR003527; MAP_kin.
TotalFoot IPR002290; Ser_thr_pkinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF00069; pkinase; 1.
ProDom; PP000001; Euk_pkinase; 1.
PROBMAT; SM00220; S_TKC; 1.
PROSITE; PS01351; MAPK; 1.
PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRO-RICH 1.
POLY-ARG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRO-RICH 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       806 AA; 87732 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         700
69
84
                                                                                                                                                                                Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
nes 70; Conserva
                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                 NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Phosphorylation
                                                                                                                                                                                                                                                                                                                                                                                                                                         nucleus.";
                                                                                                                                            MAPK7 OR ERKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NP_BIND
BINDING
ACT_SITE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4OD_RES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -!- SUBCELLULAR LOCATION: NUCLEAR.
-!- ALTERRATIVE PRODUCTS: 2 ISOFORMS; A AND B (SHOWN HERE); ARE PRODUCED BY ALTERNATIVE SPLICING.
-!- DOMAIN: COMPOSED OF THREE DOMAINS: A MODULATING N-TERMINAL DOMAIN, A DNA-BINDING DOMAIN AND A C-TERMINAL SPEROID-BINDING DOMAIN.
-!- SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTOR FAMILY.
                                                                              ARAEAQEAEDQQARVLAQLLRVWGAPR----NSDPALGL---DDDPDAPAAQLARALL-- 141
                                                                                                     --RARLDPAALAAQLVPAPVPAAALRPRPPVYDDGPAGPDAEEAGDETPDVDPELLRYLL 199
                                                                                                                                                                                                                                                                                 ----AGSIPGPASQPVCPP-----PGPVPQPAGPIPAPLQT-----APSTSLLA 655
                                    -----EGAISDNTKAALKAALLKSLRSRLRDGPSAPLEAPEPRKPVTAQERQREREEK 520
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              U., Tora L., Gronemeyer H.,
--EROER 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Two distinct estrogen-regulated promoters generate transcripts encoding the two functionally different human progesterone receptor forms A and B.";
                                                                                                                                                                                                                                           GRILAGSAD --- SEGVAAPRRLRRAADHDVGSELPPEGVLGALLRVKRLETPAPQ --- VP
                                                                                                                                                                                                   572 WIRMARPPAP-----APAPAPAPAPSSAQPISTPTGPVSQSTGPLQP-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
MEDLINE=87184565; PubMed=3551956;
Misrahl M., Atger M., D'Auriol L., Loosfelt H., Meriel C.,
Fridlansky F., Gulochon-Mantel A., Galibert F., Milgrom E.;
"Complete amino acid sequence of the human progesterone receptor deduced from cloned cDNA.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Williams S.P., Sigler P.B., "Atomic structure of progesterone complexed with its receptor."; Nature 393:392-396(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Kieback D.G., Agoulnik I.U., Tong X.-W.;
Submitted (JUL-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Biochem. Biophys. Res. Commun. 143:740-748(1987):
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    X-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS) OF 682-933
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     P06401; Q9UPF7;
01-JAN-1988 (Rel. 06, Created)
16-COT-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Progesterone receptor (PR).
PGR OR NR3C3.
HOMO Saplens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      933 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-90228361; PubMed-2328727;
Kastner P., Krust A., Turcotte B., Stropp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PubMed=9620806;
SVPRGEAAGAVQELARAL - AHLLEA -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBO J. 9:1603-1614(1990)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NR3 SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=98282128;
                                                                                                                                                                                                                                                                                                                          254 ARRLLPP 260
                                                                                                                                                                                                                                                                                                                                                                656 SQSLVPP 662
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRGR_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chambon P.
                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 11
PRGR_HUMAN
                                                                                                                                                                                                                                                                                 919
                                                                            91
                                                                                                                    521
                                                                                                                                                             142
                                    468
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16;

88; Indels 115;

5 PLINGPRAGGYGLLVLLLGLFRPPPAL - CARPVKEPRGLS - AASPPLAETGAPRRFRR

34; Mismatches

Conservative

Matches

à g œ

248 PAPQVPAR 255 || | | | 286 DAPMAPGR 293

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RESULT 13
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between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12;
                                                                                                                                                                                                                                                                                                                                                                                                             C4-TYPE.
STEROID-BINDING.
NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -----PRRFRRSVPRGEAAGAVQELARALAHLLEAERQERARAEAQERAEDQQARVLAQ 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -LDPAALAAQLVPAPV-PAAAL---RPRPPVYDDGPAGPDAEEAGDETPDVDPELLRYLL 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GRILAGSADSEGVAAPRILRRAADHDVGSELPPEGVLGALL-------RVKRLET 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GPLLKGK-----PRALGGAAAGGGAAAVPPGAAAGGVALVPKEDSRFSAPRVALVEQ 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SLDGLLFPRPCQGQDPSDEKTQDQQSLSDVEGAYSRAEATRGAGGSSSSPPEKDSGLLDS 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               109 LLRVWGAP-----RNSDPALGL------144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 174 DSSGTAAAHKVLPRGLSPARQLLLPASESPHWSGAPVKPSPQAAAVEVEEEDGSESEESA 233
                                                                                                                                                                                                                                                                                                                            PROSITE; PS0001; NUCLEAR RECEPTOR; 1. Receptor; Transcription regulation; DNA-binding; Nuclear protein; Zinc-finger; Steroid-binding; Phosphorylation; Alternative splicing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9 GPR----AGGVGLLVLLLLGLFRPP-----PALCARPVKEPRGLSAASPPLAETGA--- 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GPRAPHVAGG------PPSPEVGSPLLC-RPAAGPFPGSQTSDTLPEVSAIPI 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               83;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 933;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches 127; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                G -> S (IN REF. 1).
V -> S (IN REF. 1).
Y -> S (IN REF. 1).
S -> T (IN REF. 2).
B 0414B7F1F317F8E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                           PHOSPHORYLATION (BY CK).
MISSING (IN ISOFORM A).
G -> S (IN REF. 1).
S -> T (IN REF. 1).
S -> Y (IN REF. 1).
L -> V (IN REF. 1).
                                                                                                                                                                                                                                                                                                                                                                            MODULATING, PRO-RICH. NUCLEAR RECEPTOR-TYPE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8.6%; Score 113.5; DB 1; 23.7%; Pred. No. 2.8; ative 25; Mismatches 127;
                                                                                                                                                                                   InterPro; IPR000536; Hormone_rec_lig.
InterPro; IPR00128; Progest_receptor.
InterPro; IPR001123; Stdhrmn_receptor.
InterPro; IPR001628; Znf_C4steroid.
Pfam; PF00104; hormone_rec; 1.
Pfam; PF00105; zf-C4; 1.
Pfam; PF00105; zf-C4; 1.
PRIMTS; PR00398; STRDHORMONER.
PRINTS; PR000047; STROIDFINGER.
PRODOM; PD0000055; Znf_C4steroid; 1.
                                                                            EMBL; X51730; CAA36018.1; -.
EMBL; M15716; AAA60081.1; -.
EMBL; AF016581; AAD01587.1; -.
PIR; A03245; QRHUP.
PIR; S09971; S09971.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  98994 MM;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   232
552
793
164
                                                                                                                                                                Genew; HGNC:8910; PGR.
                                                                                                                                        PDB; 1A28; 15-JUL-98.
TRANSFAC; T00696; -.
                                                                                                                                                                                                                                                                                                       SMART; SM00430; HOLI;
SMART; SM00399; ZNF_C
                                                                                                                                                                                                                                                                                                                                                                                                           6603
183
183
2227
232
532
793
793
1 1 226
344
660
933 AA,
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                                                                                                                                                                                                                                                                                                                                                                  D-structure
                                                                                                                                                                            264080;
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DNA_BIND
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VARSPLIC
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ZN_FING
DOMAIN
MOD_RES
MOD_RES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-88274327; PubMed=2839594;
McGeoch D.J., Dalrymple M.A., Davison A.J., Dolan A., Frame M.C.,
McNab D., Perry L.J., Scott J.E., Taylor P.;
"The complete DNA sequence of the long unique region in the genome of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             92 RAEAQEAEDQQAR---VLAQLLRVWGAPRNSDPALGLDDDPDAPAQLARALLRARLDPA 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            149 ALAAQLVPAPVPAAALRPRPPVYDDGPAGPDAEEAGDE------TPDVDPELL 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      196 RYLLGRILAGSADSEGVAAPRRLRRAADHDVGSELPPEGVLGALLRVKRLET-PAPQVPA 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          41 RGLSAASPPLAETGAPRRFRRSVPRGEAAGAVQELARALAHLLEAERQ------ERA 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                herpes simplex virus type 1.";
J. Gen. Virol. 69:1531-1574(1988).
-!- FUNCION: TEGUMENT PROTEIN.
-!- SIMILARITY: BELONGS TO FAMILY THAT GROUPS TOGETHER HSV-1 UL36,
EHV-1 24, EBV BPLE1, HVS-1 64, VZV 22, AND HCMV UL48.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           |: :: ||||| | ||:| |
936 RS-IRDINDQQARRSSGLAELRRFDAL----DAALGQQLDSDA---------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 3164;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2911 2980 35 X 2 AA TANDEM REPEATS OF P-Q. 3164 AA; 335857 MW; CC5D31FF4F9FE3F4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8.6%; Score 113.5; DB 1; Length: 26.9%; Pred. No. 9.4; ive 23; Mismatches 95; Indels
                                                                                                                                                                                                              Herpes simplex virus (type 1 / strain 17).
Viruses; dSDNA viruses, no RNA stage; Herpesviridae;
Alphaherpesvirinae; Simplexvirus.
                                                                                01-MAR-1989 (Rel. 10, Last sequence update)
01-APR-1993 (Rel. 25, Last annotation update)
Large tegument protein (Virlon protein UL36).
   3164 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR005210; Herpes_UL36.
                                                          01-MAR-1989 (Rel. 10, Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; X14112; CAA32311.1; -. PIR; I30085; WMBEH6.
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Best Local Similarity 26.99
Matches 66; Conservative
STANDARD;
                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                               NCBI_TaxID=10299;
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TEGU_HSV11
P10220:
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ESTABLISHING A SIGNALING COMPLEX FOR DOPAMINERGIC
NEUROTRANSMISSION THROUGH D2 RECEPTORS BY LINKING RECEPTORS
DOWNSTREAM SIGNALING MOLECULES AND THE ACTIN CYTOSKELETON.
SUBUNIT: POSSIBLY EXISTS AS AN HOMODIMER, HOMOTRIMER OR AN
HOMOTETRAMER. INTERACTS WITH F-ACTIN, PROTEIN PHOSPHATASE 1 (PP1)
NEURABIN-1, TGN38 AND D(2) DOPAMINE RECEPTOR.
                                                                                                                                                                                                                                                                Allen P.B., Ouimet C.C., Greengard P.; "Spinophilin, a novel protein phosphatase 1 binding protein localized
                                                                                                                                              Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE OF 100-767 FROM N.A., AND INTERACTION WITH D2DR.
MEDLINE-99321921; PubMed-10391935;
Smith F.D., Oxford G.S., Milgram S.L.;
"Association of the D2 dopamine receptor third cytoplasmic loop with spinophalia, a protein phosphatase-1-interacting protein.";
J. Biol. Chem. 274:19894-19900(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Brain actin-associated protein phosphatase 1 holoenzymes containing spinophilin, neurabin, and selected catalytic subunit isoforms."; J. Biol. Chem. 274:35845-35854(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                    Hirao K., Nishioka H., Hata Y., Mizoguchi A., Takai Y.;
"Neurabin-Ir/spinophilin. An actin filament-binding protein with one
goz domain localized at cadherin-based cell-cell adhesion sites.";
J. Biol. Chem. 273:3470-3475(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                 Satoh A., Nakanishi H., Obaishi H., Wada M., Takahashi K., Satoh K.,
                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A., AND SEQUENCE OF 4-24; 164-182; 199-242; 449-480;
                              16-OCT-2001 (Rel. 40, Last sequence update)
15-UN-2002 (Rel. 41, Last aequence update)
15-UN-2002 (Rel. 41, Last annotation update)
Neurabin-II (Neural tissue-specific F-actin binding protein II)
(Protein phosphatase 1 regulatory subunit 9B) (Spinophilin) (p130)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-99445568; PubMed-10514494;
Stephens D.J., Banting G.;
"Direct interaction of the trans-Golgi network membrane protein,
TGN38, with the F-actin binding protein, neurabin.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MacMillan L.B., Bass M.A., Cheng N., Howard E.F., Tamura M., Strack S., Wadzinski B.E., Colbran R.J.;
                                                                                                                                                                                                                                                                                                                Proc. Natl. Acad. Sci. U.S.A. 94:9956-9961(1997).
 817 AA.
PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=20054471; PubMed=10585469;
                                                                                                                                                                                                                                                 MEDLINE=97420791; PubMed=9275233;
                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-98123121; PubMed-9452470;
 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INTERACTION WITH TGN38.
                                                                                                                                                                                                                                                                                                                                                                    578-689 AND 776-791.
                                                                                                                                                                                                                                                                                                   dendritic spines.
                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                               NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CHARACTERIZATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    rissue-Brain;
                                                                                                                                                                                                                                                                                                                                                                                  ISSUE-Brain;
                                                                                                               PP1bp134).
 NEB2_RAT
035274;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12;
SUBCELLULAR LOCATION: ENRICHED AT SYNAPSE AND CADHERIN-BASED CELL-CELL ADHESION SITES.

TISSUE SPECIFICITY: UBIQUITOUS. ABUNDANTLY EXPRESSED IN THE BRAIN. EXPRESSED AT HIGHEST LEVELS IN HIPPOCAMPUS AND AT LOWER LEVELS IN THE CORTEX, CEREBELLUM AND BRAINSTEM. LOCALIZES TO THE DENDRITIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRASSLNENVDHSALLKLGTSVSERVSRFDSKPAPSAQPAPPH-----PPSRLQETRK 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RFRRSVPRGEAAGAVQELARALAHLLEAERQERARAEAQEAE------D 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LFERSVP-AASGGDKEAVARRIL-----RQERASLQDRKLDVVVRFNGSTEALDKLDAD 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 101 QQARVLAQLLRVWGAPRNSDPALGLDDDPDAP----AAQLARALLRARLDPAALAAQLVP 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         157 APVPAAALRPRPPVYDDGPAG - PDAEEAGDETPDVDPELLRYLLGRILAGSADSEGVAA 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PPPPPAPSGDAATEKDRGPGGQOPQHRVAPARPPPKPREVRKIKPVEVEESGESEAESA 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRAGGVGLLV----LLLLGL-----FRPPPALCARPVKEPRGLSAASPPLAETGAPR 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MISSING: ABOLISHES PROTEIN PHOSPHATASE
                                                                                                                                                                           - DEVELOPMENTAL STAGE: EXPRESSION IS LOW DURING EMBRYOGENESIS AND INCREASES AROUND POSTNATAL DAY 21.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COILED COIL (POTENTIAL).
COILED COIL (POTENTIAL).
INTERACTS WITH D(2) DOPAMINE RECEPTOR.
INTERACTS WITH PROTEIN PHOSPHATASE 1.
INTERACTS WITH TGN38.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             F->A: ABOLISHES PROTEIN PHOSPHATASE BINDING.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
01-FEB-1996 (Rel. 33, Last annotation update)
Large proline-rich protein BAT2 (HLA-B-associated transcript 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           72;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 112; DB 1; Length 817;
Pred. No. 3.1;
8; Mismatches 120; Indels '
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cytoskeleton; Coiled coil.
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Pfam; PF00595; PDZ; 1.
SMART; SM00228; PDZ; 1.
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665
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P48634;
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Best Local
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MEDLINE-97250498; PubMed-9096354; Wise C.A., Chiang L.C., Paznekas W.A., Sharma M., Musy M.M., Ashley J.A., Lovett M., Jabs E.W.; "TCCF1 gene encodes a putative nucleolar phosphoprotein that exhibits mutations in Treacher Collins syndrome throughout its coding region.";
                                                                                                                                                                                                              85 AERQERARAEAQEAEDQQARVLAQLLRVWGAPRNSDP-----ALGLDDDPDAPAAQLA 137
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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MEDLINE-96154183; PubMed-9563749;
Dixon J., Edwards S.J., Gladwin A.J., Dixon M.J., Loftus S.K.,
Bonner C.A., Koprivnikar K., Wasmuth J.J.;
"Postitonal cloning of a gene involved in the pathogenesis of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-97228900; PubMed-9074926;
Dixon J., Edwards S.J., Anderson I., Brass A., Scambler P.J.,
Dixon M.J.;
                                                                                                                         8.4%; Score 111; DB 1; Length 2142;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Identification of the complete coding sequence and genomic organization of the Treacher Collins syndrome gene."; Genome Res. 7:223-234(1997).
   1068 M -> L (IN REF. 2).

1285 P -> R (IN REF. 2).

1400 G -> A (IN REF. 2).

1511 T -> S (IN REF. 2).

1729 G -> A (IN REF. 2).

1729 G -> A (IN REF. 2).

AA; 227840 MW; 32DDF16B9B52420A CRC64;
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01-NOV-1997 (Rel. 35, Last sequence update)
15-UTNV-2002 (Rel. 41, Last annotation update)
Treacle protein (Treacher collins syndrome protein).
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30; Mismatches
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Q13428; Q99408;
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                                                                                                                    TISSUE=T-cell;
MEDIINE=90192810; PubMed=2156268;
Banacril J., Sands J., Strominger J.L., Spies T.;
"A gene pair from the human major histocompatibility complex encodes large proline-rich proteins with multiple repeated motifs and a single ubiquitin-like domain.";
Proc. Natl. Acad. Sci. U.S.A. 87:2374-2378(1990).
                                                                                                                                                                                                                                                    SEQUENCE OF 1-1860 FROM N.A.
MEDILINE-91272029; PubMed-8499947;
Iris F.J.M., Bougueleret L., Prieur S., Caterina D., Primas G.,
Perrot V., Jurka J., Rodriguez-Tome P., Claverie J.-M., Dausset J.,
Cohen D.,
                                                                                                                                                                                                                                                                                                                                      "Dense Alu clustering and a potential new member of the NF kappa B family within a 90 kilobase HLA class III segment.";
Nat. Genet. 3:137-145(1993).
-1- FUNCTION: UNKNOWN.
                                Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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EMBL; M33518; AAA35586.1; -.
EMBL, M33512; AAA35586.1; JOINED.
EMBL; 215025; CAA78744.1; -.
PIR; B35098; B35098.
PIR; S36152; S36152.
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                   Homo sapiens (Human).
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                                                                   NCBI_TaxID=9606;
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                                                                                  AM. J. Hum. Genet. 60:515-524(1997).

-1- DISEARS: DEPECTS IN TCOF1 ARE THE CAUSE OF TREACHER COLLINS
SYNDROME (TCS). TCS IS A AUTOSOMAL DOMINANT DISORDER OF
CRANIOPACIAL DEVELOPMENT THAT OCCURS WITH AN INCIDENCE OF 1/50,000
LIVE BIRTHS. THE CLINICAL FRATURES OF TCS ARE BILATERALLY
SYMMETRICAL AND INCLUDE: (1) ABNORMALITIES OF THE EXTERNAL EARS,
ATRESIA OF THE EXTERNAL EAR CANALS, AND MALPORMATION OF THE MIDDLE
EAR OSSICLES, WHICH MAY RESULT IN CONDUCTIVE HEARING LOSS; (2)
LATERAL DOWNWARD SLOPING OF PALPEBRAL FISSURES, FREQUENTLY WITH
COLOBOMAS OF THE LOWER EXELLIDS; (3) HYPOPLASIA OF THE MANDIBLE AND
ZYGOMATIC COMPLEX; (4) CLEFT PALATE.
                  VARIANTS L-439; V-810; V-1313 AND G-1355, AND VARIANT TCS R-53. MEDLINE-97195537; PubMed-9042910; Bdwards S.J., Gladwin A.J., Dixon M.J.; "The mutational spectrum in Treacher Collins syndrome reveals a predominance of mutations that create a premature-termination
Proc. Natl. Acad. Sci. U.S.A. 94:3110-3115(1997).
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                                                                                                                                                                                                                                                                                                      88;
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                                                                                                                                                                                                                                                                                                     80; Indels
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K -> Q (IN REF. 2).
W; 3880203D985c2699 CRC64;
                                                                                                     POLY-LYS.
POLY-LYS.
W -> R (IN TCS).
/FTId-VAR_005630.
P -> L.
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/FTId=VAR_005633.
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A -> V.
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                                                                               POLY-SER.
POLY-LYS.
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                                      Polymorphism.
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InterPro; IPR003993; treacle.
Pfam; PF03546; treacle; 3.
PRINTS; PR01503; TREACLE.
                                                                                                                                                                                                                                                                                                     56; Conservative
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SEQ ID NO 78
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                                                             4, 2003, 14:15:40 ; Search time 15 Seconds (without alignments) 509:997 Million cell updates/sec
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/cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
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/cgn2_6/ptodata/1/iaa/PcTUS_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PcTUS_COMB.pep:*
        GenCore version 5.1.4_p5_4578
Copyright (c) 1993 - 2003 Compugen Ltd.
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US-08-470-335-210

US-08-467-602-404

US-08-467-602-382

US-08-467-602-384

US-08-470-339-189

US-08-470-339-189

US-08-470-339-189

US-08-48-926-3

US-08-48-926-3

US-08-428-927-3

US-08-438-927-3

US-08-438-927-3

US-08-438-927-3

US-08-438-927-3

US-08-438-927-3

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US-08-438-927-3

US-08-438-927-3

US-08-438-927-3
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Maximum Match 100%
Listing first 45 summaries
                                              protein search, using sw model
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length: 2000000000
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APPLICANT: Gesellschaft fuer Biotechnologische Forschung mbH
APPLICANT: Bristol-Myers Squibb, Co.
APPLICANT: Beyer, Stefan
APPLICANT: Bloecker, Helmut
APPLICANT: Brandt, Petra
APPLICANT: Cino, Paul M
APPLICANT: Coldberg, Steven L
APPLICANT: Goldberg, Steven L
APPLICANT: Hofle, Gerhard
APPLICANT: Feichenbach, Hans
TITLE OF INVENTION: heteropolyketide compounds
TITLE OF INVENTION: heteropolyketide compounds
FILE REFERENCE: PCT/VO 99/23535
CURRENT FILING DATE: 1999-10-07
ERALIER FILING DATE: 1999-10-07
ERALIER FILING DATE: 1998-10-09
NUMBER OF SEQ ID NOS: 107
SOFTWARE: PatentIn Ver. 2.1
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US-08-467-602-324
PCT-US94-05083C-166
PCT-US94-05083C-185
PCT-US94-05083C-185
PCT-US94-05083C-185
US-08-470-335-226
US-08-467-602-328
US-08-467-602-328
US-08-467-602-303
US-08-467-602-365
US-08-467-602-365
US-08-467-602-365
US-08-467-602-365
US-08-467-602-365
US-08-467-602-365
US-08-467-602-365
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; Pred. No. 0.00031;
13; Mismatches 72;
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US-08-467-602-370
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; Sequence 78, Application US/09413814
; Patent No. 6225064
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Best Local Similarity 27.2%
Matches 71; Conservative
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                                                                                                                      DB 4; Length 248;
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TITLE OF INVENTION: PREPARATION AND USE
FILE REFERENCE: 04585/002008
CURRENT APPLICATION NUMBER: US/08/470,339C
CURRENT FILING DATE: 1995-06-06
EARLIER PILING DATE: 1993-03-24
EARLIER FILING DATE: 1993-09-03
EARLIER FILING DATE: 1992-09-03
EARLIER FILING DATE: 1992-06-30
EARLIER FILING DATE: 1992-06-30
EARLIER FILING DATE: 1992-06-30
EARLIER FILING DATE: 1992-04-03
                                                                                                                   ; Score 119.5; DB 4;
; Pred. No. 0.0026;
15; Mismatches 66;
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28.0%; Pred. No. 0.0026;
ive 15; Mismatches 66;
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SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; Sequence 210, Application US/08470339C; Patent No. 6232286; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: STROOBARY, PAUL
APPLICANT: MINGHETTI, LUISA
APPLICANT: WATERFIELD, MICHAEL
APPLICANT: MARCHIONNI, MARK
APPLICANT: CHEN, MARIO S.
APPLICANT: HILES, IAN
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Best Local Similarity 28.0%;
Matches 56; Conservative 1
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Best Local Similarity 28.0
Matches 56; Conservative
                    ; TYPE: PRT
; ORGANISM: Homo sapiens
US-08-470-335-210
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ORGANISM: Homo sapiens
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US-08-470-339-210
LENGTH: 248
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LENGTH: 248
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           66; Indels
                                                                                                                                                                                                                                                      APPLICANT: Gymne, David I.

APPLICANT: Gymne, David I.

APPLICANT: Mahanthappa, Nagesh K.

APPLICANT: Marchland: Mark A.

APPLICANT: Barningham-WcDonogh, Olivia
APPLICANT: Goldin, Stanley M.

APPLICANT: McBurney, Robert N.

TITLE OF INVENTION: USE OF NEUREGULINS AS MODULATORS OF
TITLE OF INVENTION: CELLULAR COMMUNICATION
FILE REFERENCE: 04585/041001
CURRENT APPLICATION UNMBER: US/08/341,018A
CURRENT FILING DATE: 1994-11-17
NUMBER OF SEQ ID NOS: 87

SOFTWARE: FASTESQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: GLIAL MITOGENIC FACTORS, THEIR TITLE OF INVENTION: PREPARATION AND USE
FILE REFERENCE: 04585/00200B
CURRENT APPLICATION NUMBER: US/08/470,335F
CURRENT FILING DATE: 1995-06-06
EARLIER APPLICATION NUMBER: 08/036,555
BARLIER FILING DATE: 1993-03-24
NUMBER OF SEQ ID NOS: 252
SOFTWARE: FESSES for Windows Version 4.0
SEQ ID NO 210
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9.1%; Score 119.5; DB :
Best Local Similarity 28.0%; Pred. No. 0.0026;
Matches 56; Conservative 15; Mismatches 6
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                                                                                                                                                                                Sequence 52, Application US/08341018A Patent No. 6087323 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  107 EAGAWGG-------DREPPAA---
                 235 VLGALLRVKRLETPAPQVPAR 255
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APPLICANT: STROODSNAT, PAUL
APPLICANT: MINGHERT! LUISA
APPLICANT: WATERFIELD, MICHAEL
APPLICANT: MATERFIELD, MICHAEL
APPLICANT: CHEN, MARK
APPLICANT: CHEN, MARIO S.
APPLICANT: HILES, IAN
                                                                 721 ----- 721 ----- 728
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US-08-341-018-52
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LENGTH: 248
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109 ILLRVWGAPRNSDPALGLDDDPDAPAQLARALLRARLDPAALAAQLVPAPVPAAALRPRP 168
                                       ----GPRALGP---PAEEPLLAANGTV 140
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        67 P-----SVGSVQELAQRAAVVIEGKVHPQRR--QQGALDRKAAAAG 106
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                                                                                                                                                                                                            Sequence 207, Application US/08467602C

Patent No. 6444642

GENERAL INFORMATION:
APPLICANT: SALA: Robert
APPLICANT: MATCHIONI, MATK
APPLICANT: GANDE, David I.
TILLE OF INVENTION: DISONDERS
FILE REFERENCE: 04585/028003

CURRENT FILING DATE: 1994-03-08

EARLIER APPLICATION NUMBER: 08/059,204

EARLIER APPLICATION NUMBER: 08/059,022

EARLIER PILING DATE: 1994-03-08

EARLIER PILING DATE: 1993-05-06

NUMBER OF SEQ ID NOS: 420

SOFTWARRE: FastSEQ for Windows Version 4.0

LENGTH: 248
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APPLICANT: SKIAT, Robert
APPLICANT: Warchionn1, Mark
APPLICANT: Gwynne, David I.
TITLE OF INVENTION: METHODS FOR TREATING MUSCLE DISEASES AND
TITLE OF INVENTION: DISORDERS
FILE REPREBENCE: 04585/02803
CURRENT PILING DATE: 1995-06-06
EARLIER APPLICATION NUMBER: 08/209,204
EARLIER FILING DATE: 1994-03-08
EARLIER FILING DATE: 1993-06-06
EARLIER FILING DATE: 1993-05-06
HOWER OF SEQ ID NOS: 420
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28.0%; Pred. No. 0.0026;
tive 15; Mismatches 66;
                                     107 EAGAWGG-----DREPPAA----
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                                                                             169 PVYDDGPAGPDAEEAGDETP 188
                                                                                                                    141 PSWPTAPV-PSAGEPGEEAP 159
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hes 56; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; TYPE: PRT
; ORGANISM: Homo sapiens
US-08-467-602-207
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US-08-467-602-207
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                                                                                                                                                        ; Score 119.5; DB 4;
; Pred. No. 0.0026;
15; Mismatches 66;
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APPLICANT: WARGHONI, MARK
APPLICANT: CHEN, MARIO S.
APPLICANT: HILES, IAN
TITLE OF INVENTION: GLIAL MITOGENIC FACTORS, THEIR
TITLE OF INVENTION: PREPARATION AND USE
FILE REFERENCE: 04585/00200B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9.1%; Score 119.5; DB 4;
28.0%; Pred. No. 0.004;
tive 15; Mismatches 66;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/08/470,335F
CURRENT FILING DATE: 1995-06-06
EARLIER APPLICATION NUMBER: 08/036,555
EARLIER FILING DATE: 1993-03-24
NUMBER OF SEQ ID NOS: 252
SOFTWARE: FASTSEQ for Windows Version 4.0
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 188, Application US/08470335F Patent No. 6147190
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                                                                                                                                                        Query Match
Best Local Similarity 28.0%;
Matches 56; Conservative 15
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ORGANISM: Homo sapiens
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Best Local Similarity
Matches 56; Conserv
                                                                                       Homo
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                                                                                                             US-08-467-602-404
                     SEQ ID NO 404
LENGTH: 248
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                                                                                         ORGANISM:
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49 PLAETGAPRRFRRSVPRGEAAGAVQELARALAHLLEAERQERARAEAQEAEDQQARVLAQ 108
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                                                                                                                                                                                                                                                                                                                                                                     Query Match
9.1%; Score 119.5; DB 4; Length 405;
Best Local Similarity 28.0%; Pred. No. 0.0048;
Matches 56; Conservative 15; Mismatches 66; Indels 63.
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                                                                           ) ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: VARIANT

LOCATION: (34)...(34)

OTHER INFORMATION: Xaa is any amino acid

US-08-467-602-384
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APPLICANT: GOODEARL, ANDREW
APPLICANT: STROOBANT, PAUL
APPLICANT: WATERFIELD, MICHAEL
APPLICANT: WATERFIELD, MICHAEL
APPLICANT: MATERFIELD, MICHAEL
APPLICANT: CHEW, MARK
APPLICANT: CHEW, MARK
APPLICANT: HILES, IAN
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175 PSWPTAPV-PSAGEPGEEAP 193
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US-08-470-339-189
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ORGANISM:
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                                                                                                                                                                                                                                                                                                              APPLICANT: SCAILT, Robert
APPLICANT: Marchionni, Mark
APPLICANT: Gwynne, David I.
TITLE OF INVENTION: METHODS FOR TREATING MUSCLE DISEASES AND
TITLE OF INVENTION: DISORDERS
FILE REFERENCE: 04585/028003
CURRENT APPLICATION NUMBER: 08/08/467,602C
CURRENT FILING DATE: 1995-06-06
EARLIER FILING DATE: 1994-03-08
EARLIER RILING DATE: 1994-03-08
EARLIER FILING DATE: 1994-03-08
NUMBER OF SEQ ID NOSE: 1993-05-06
NUMBER OF SEQ ID NOSE: 1993-05-06
SOFTWARE FEALSOR FOR WINDOWS VERSION 4.0
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APPLICANT: Stlar, Robert
APPLICANT: Stlar, Robert
APPLICANT: GWYDNE, David I.

ITILE OF INVENTION: DESCRIBES
ITILE OF INVENTION: DISCRIBES
ITILE OF INVENTION: DAVID INSCRIBES
ITILE OF INVENTION: DAVID INV
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LOCATTON: (34)...(34)

COTHER INFORMATION: Xaa is any amino acid
US-08-467-602-382
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                                                                                                                                                                                             Sequence 382, Application US/08467602C Patent No. 6444642 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 384, Application US/08467602C Patent No. 6444642
141 PSWPTAPV-PSAGEPGEEAP 159
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Best Local Similarity 28.0%
Matches 56; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-467-602-384
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GENERAL INFORMATION:
APPLICANT: Goodea
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                PLAETGAPRRFRRSVPRGEAAGAVQELARALAHLLEAERQERARAEAQEAEDQQARVLAQ 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          49 PLAETGAPRRFRRSVPRGEAAGAVQELARALAHLLEAERQERARAEAQEAEDQQARVLAQ 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          109 LLRVWGAPRNSDPALGLDDDPDAPAAQLARALLRARLDPAALAAQLVPAPVPAAALRPRP 168
                                                                                       107 EAGAWGG-------DREPPAA-----GPRALGP---PAEEPLLAANGTV 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      109 ILRVWGAPRNSDPALGLDDDPDAPAAQLARALLRARLDPAALAAQLVPAPVPAAALRPRP 168
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9.1%; Score 119.5; DB 4; Length 414; 28.0%; Pred. No. 0.0049; tive 15; Mismatches 66; Indels 63
                                                                                                                                                                                                                                           Patent No. 6232286
GENERAL INFORMATION:
APPLICANT: GOODEARL, ANDREW
APPLICANT: STROCOBART, PAUL
APPLICANT: WINGHETTI, LUISA
APPLICANT: WARCHIONNI, WARK
APPLICANT: CHEN, MARCHIONNI, WARK
APPLICANT: CHEN, MARIO S.
APPLICANT: HILES, IAN
TITLE OF INVENTION: GLIAL MITOGENIC FACTORS, THEIR
TITLE OF INVENTION: PREPARATION AND USE
FILE REFERENCE: 04585/002008
                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 12
US-08-036-555B-170
; Sequence 170, Application US/08036555B
; Patent No. 5530109
                                                                                                                                                                                                                              Sequence 188, Application US/08470339C
Patent No. 6232286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   107 EAGAWGG-----DREPPAA
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Best Local Similarity 28.09
Matches 56; Conservative
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ORGANISM: Homo sapiens
US-08-470-339-188
                                                                                                                                                                                                RESULT 11
US-08-470-339-188
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49 PLAETGAPRRFRRSVPRGEAAGAVQELARALAHLLEAERQERARAEAQEAEDQQARVLAQ 108
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APPLICANT: Goodearl, Andrew; Stroobant, Paul;
APPLICANT: Minghetti, Luisa; Waterfield, Michael; Marchioni, Mark;
APPLICANT: Chen, Maio Su; Hiles, Ian
TITLE OF INVENTION: Glial Mitogenic Factors, Their
TITLE OF INVENTION: Preparation and Use
NUMBER OF SEQUENCES: 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9.1%; Score 119.5; DB 1; Length 422; 28.0%; Pred. No. 0.0051; tive 15; Mismatches 66; Indels 63
                                                                                                                                                                                                                                                                                                                                                                                                               Diskette, 5.25 inch, 360 kb storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATE:

APPLICATION NUMBER: 07/863,703
FILING DATE: 03-APRIL-1992
PRIOR APPLICATION NUMBER: 0.7/865.3
PRIOR APPLICATION DATE: 0.8-APRIL-1991
APPLICATION NUMBER: 0.K. 91 07566.3
FILING DATE: 10-APRIL-1991
ATTORNEY/AGENT INFORMATION:
REGISTRENCE/DOCKET NUMBER: LUD 5250.4
FELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION SEG 120 689-9200
TELECOMMUNICATION SEG 120 689-3804
INFORMATION FOR SEG 1D NO: 170:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/036,555B
FILING DATE: 24 MAR-1993
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/965,173
FILING DATE: 23-0CT-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/940,389
FILING DATE: 03-SEP-1992
PRIOR APPLICATION DATA:
FILING DATE: 30-JUN-1992
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ADDRESSEE: Felfe & Lynch
STREET: 805 Third Avenue
CITY: New York City
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OPERATING SYSTEM: PC-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 28.0%
Matches 56; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; TOPOLOGY: linear
US-08-036-555B-170
                                                                                                                                                                                                                                                                                                           New York
                                                                                                                                                                                                                                                                                                                                                                                                                                              IBM
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Indels
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COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; Score 119.5; DB
; Pred. No. 0.0051;
15; Mismatches 6
                                                                                                                                                                                                                                                                                                                                                  STREET: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/428,926
FILING DATE: 25-APR-1995
                                                                                                                                                                                                                   Sequence 3, Application US/08428926 Patent No. 5667780
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/339517
FILING DATE: 14-NOV-1994
ATTORNEY/AGENT INFORMATION:
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NAME: Lee, Wendy M.
REGISTRATION NUMBER: 00,000
REFERENCE/DOCKET NUMBER: 853
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-1994
TELEFAX: 415/952-9881
                                                              169 PVYDDGPAGPDAEEAGDETP 188
                                                                                                       141 PSWPTAPV-PSAGEPGEEAP 159
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PSWPTAPV-PSAGEPGEEAP 159
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Best Local Similarity 28.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-428-926-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: Goodearl, Andrew: Stroobant, Paul;
APPLICANT: Goodearl, Luisa: Waterfield, Michael; Marchioni, Mark;
APPLICANT: Chen, Maio Su; Hiles, Ian
TITLE OF INVENTION: Gial Mitogenic Factors, Their
TITLE OF INVENTION: Preparation and Use
NUMBER OF SEQUENCES: 184
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               63;
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                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
COMPUTER: IBM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/469,569
FILING DATE: 06-JUN-1995
CLASSIFTCATION DATA:
APPLICATION NUMBER: 08/036,555
FILING DATE: 24-MAR-1993
APPLICATION NUMBER: 07/965,173
FILING DATE: 23-OCT-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/940,389
FILING DATE: 03-SEP-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/940,389
FILING DATE: 03-SEP-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/970,138
FILING DATE: 30-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
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FILING DATE: 03-APRIL-1992
PRIOR APPLICATION DATA:
PAPPLICATION NUMBER: U.K. 91 07566.3
FILING DATE: 10-APRIL-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Tsal, Christine H.
REGISTRATION NUMBER: 34,266
REFERNCE/DOCKET NUMBER: LUD 5250.4
TELECOMMUNICATION:
TELEPHONE: (212) 688-9200
                                                       Sequence 170, Application US/08469569
Patent No. 5606032
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: (212) 838-3884
INFORMATION FOR SEQ ID NO: 170:
                                                                                                                                                                                                                                                                             ADDRESSEE: Felfe & Lynch
STREET: 805 Third Avenue
CITY: New York City
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OPERATING SYSTEM: PC-DOS
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Best Local Similarity 28.0%
Matches 56; Conservative
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LENGTH: 422
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; TOPOLOGY: linear
US-08-469-569-170
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             RESULT 13
US-08-469-569-170
                                                                                                                                                                                                                                                                                                                                                                      COUNTRY:
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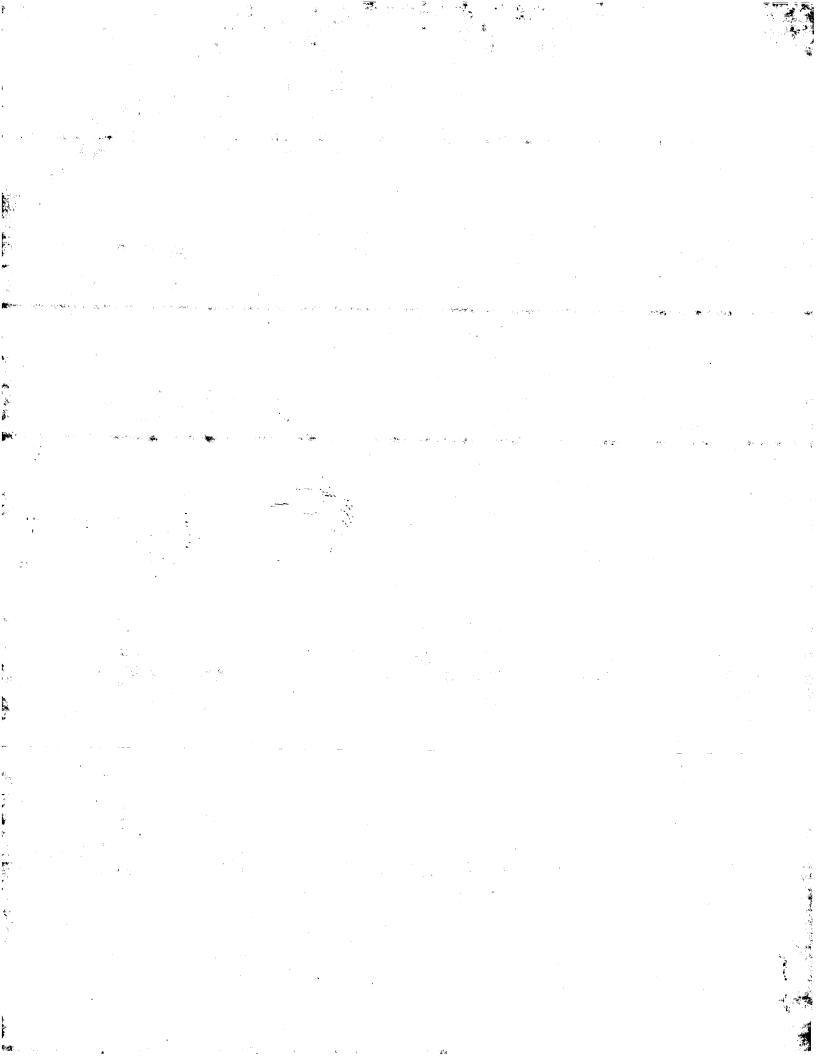
---GPRALGP---PAEEPLLAANGTV 140 ---GPRALGP---PAEEPLLAANGTV 140 49 PLAETGAPRFFRSVPRGEAAGAVQELARALAHLLEAERQERARAEAQEAEDQQARVLAQ 108 67 P------GGALDRKAAAAG 106 109 LLRVWGAPRNSDPALGLDDDPDAPAAQLARALLRARLDPAALAAQLVPAPVPAAALRPRP 168 2 AGSPLLWGPRAGGVG------LLVLLLLGLFRPPPALCARPVKEPRGLSA--ASP 48 GENERAL INFORMATION:
APPLICANT: Ho, Wei-Hsien
APPLICANT: OSheroff, Phyllis L.
TILLE OSHEROFF, SENSORY AND MOTOR NEURON DERIVED FACTOR (SMDF)
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSES:
GENERAL INFORMATION:
ADDRESSES:
AD Length 422;

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109 LLRVWGAPRNSDPALGLDDDPDAPAAQLARALLRARLDPAALAAQLVPAPVPAAALRPRP 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   49 PLAETGAPRRFRRSVPRGEAAGAVQELARALAHLLEAERQERARAEAQEAEDQQARVLAQ 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10 SGRP---GPRAORPGSAARSSPPLPLLLLLLGTAALAPGAAAGNEAAPAGASVCYSSP 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
COMPUTER: IBM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/036,555
FILING DATE: 24-MAR-1993
PRIOR APPLICATION NUMBER: 08/036,555
FILING DATE: 23-0CT-1992
FILING DATE: 23-0CT-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/940,389
FILING DATE: 03-SEP-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/907,138
FILING DATE: 30-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/863,703
FILING DATE: 03-APRIL-1992
PRIOR DATE: 03-APRIL-1993
ATPONEY APPLICATION NUMBER: 07-861,703
FILING DATE: 10-APRIL-1991
ATPONEY APPLICATION NUMBER: 07-861,703
ANNUMBER: 07-861
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REGISTRATION NUMBER: LUD 250.4
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 688-9200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US/08/249,322A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OPERATING SYSTEM: PC-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                28.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/08
FILING DATE: 26-MAY-1994
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 9.1%
Best Local Similarity 28.0%
Matches 56; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Wordperfect CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
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US-08-249-322A-170
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                                                                                                                                US-08-249-322A-170
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Search completed: April 4, 2003, 14:18:57 Job time: 17 secs



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April 4, 2003, 14:18:20 ; Search time 36 Seconds (without alignments) 441.538 Million cell updates/sec
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1319
1 MAGSPLLWGPRAGGVGLLVL......RVKRLETPAPQVPARRLLPP 260
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/cgn2_6/ptodata/2/pubbaa/US07_PUBCOMB.pep:*
/cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep:*
/cgn2_6/ptodata/2/pubpaa/US09_RUBCOMB.pep:*
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/cgn2_6/ptodata/2/pubpaa/US09_RUB.PUB.pep:*
/cgn2_6/ptodata/2/pubpaa/US09_RUB.pep:*
/cgn2_6/ptodata/2/pubpaa/US09_RUB.pep:*
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      248812
GenCore version 5.1.4\_p5\_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         248812 segs, 61136040 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Published_Applications_AA:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                              - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                  Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Perfect score:
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                                                                                                           OM protein
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

/cgn2\_6/ptodata/2/pubpaa/US10\_PUBCOMB.pep:\* /cgn2\_6/ptodata/2/pubpaa/US60\_NEW\_PUB.pep:\* /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB.pep:\*

## SUMMARIES

	Description	Sequence 6, Appli	Sequence 14, Appl	Sequence 150, App	Sequence 238, App	Sequence 3, Appli	Sequence 3, Appli	Sequence 3, Appli	Sequence 47, Appl	Sequence 47, Appl	Sequence 47, Appl	Sequence 2, Appli	Sequence 206, App	Sequence 2, Appli	Sequence 5, Appli	Sequence 43, Appl	Sequence 43, Appl	Sequence 43, Appl	Sequence 11830, A	Sequence 2, Appli
	ID	US-09-803-589-6	US-09-803-589-14	US-09-984-271-150	US-09-984-271-238	US-09-946-807-3	US-09-795-668-3	US-09-795-686-3	US-09-976-740-47	US-10-023-529-47	US-10-023-523-47	US-09-825-288A-2	US-09-764-898-206	US-10-077-130-2	US-10-077-130-5	US-09-976-740-43	US-10-023-529-43	US-10-023-523-43	US-09-815-242-11830	US-09-858-664A-2
	DB	10	10	6	σ	0	10	10	6	12	12	σ	10	6	σ	σ	12	12	10	10
	Duery Match Length DB	260	175	149	166	418	418	418	550	550	550	1298	492	2630	7968	538	538	538	681	1665
dР	Query Match	100.0	47.5	23.4	23.4	9.4	9.4	4.6	0.6	9.0	0.6	9.0	8.7	8	8.5	8.4	8.4	8.4	8.3	8.3
	Score	1319	627	308	308	124.5	124.5	124.5	118.5	118.5	118.5	118.5	114.5	112	112	110.5	110.5	110.5	109	109
	Result No.	-	7	m	4	Ŋ	9	7	œ	o	10	11	12	13	14	15	16	17	18	19

1 MAGSPLIMGPRAGGVGLLVILLIGIFRPPPALCARPVKEPRGLSAASPPLAETGAPRRFR 60

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Sequence 3, Appli Sequence 216, App Sequence 116, App Sequence 5, Appli Sequence 6, Appli Sequence 233, App Sequence 1037, Ap Sequence 1037, Ap Sequence 313, App Sequence 31, Appli Sequence 3, Appli Sequence 6, Appli Sequence 6, Appli Sequence 6, Appli Sequence 6, Appli Sequence 6, Appli Sequence 425, App Sequence 334, App	G THERAPEUTIC AND OTHER	Length 260; ndels 0; Gaps 0;
	ALIGNMENTS  BESULT 1  US-09-803-589-6  Sequence 6, Application US/09803589  Patent No. US20020112251A1  GENERAL INFORMATION:  APPLICANT: HOLTZMAN, Sean A.  APPLICANT: GOOGARI, AND D.U.  TITLE OF INVENTION: DRESS  TITLE OF INVENTION: DRESS  TITLE OF INVENTION: DRESS  TITLE OF INVENTION: UNBER: US/09/803,589  CURRENT APPLICATION NUMBER: US 09/128,709  PRIOR APPLICATION NUMBER: US 09/128,709  PRIOR APPLICATION NUMBER: US 09/128,709  PRIOR FILING DATE: 1998-08-04  PRIOR FILING DATE: 1998-08-06  PRIOR FILING DATE: 1997-08-06  PRIOR FILING DATE: 1997-08-06  PRIOR PLING DATE: 1997-09-01  PRIOR APPLICATION NUMBER: US 60/054,966  PRIOR PLING DATE: 1997-09-01  PRIOR PLING DATE: 1997-09-01  PRIOR PLING DATE: 1997-09-01  NUMBER OF SEQ ID NOS: 14  NUMBER OF SEQ ID NOS: 14  CREATHER PRIOR DATE: 1999-09-01  NUMBER OF SEQ ID NOS: 14  TYPE: PRIOR PLING DATE: 1999-09-01  NUMBER OF SEQ ID NOS: 14  TYPE: PRIOR TITLING DATE: 1997-09-01  NUMBER OF SEQ ID NOS: 14  TYPE: PRIOR TITLING DATE: 1997-09-01  NUMBER OF SEQ ID NOS: 14  TYPE: PRIOR TITLING DATE: 1999-09-01  TYPE: PRIOR TITLING DATE: 1999-09-01  NUMBER OF SEQ ID NOS: 14  TYPE: PRIOR TITLING DATE: 1999-09-01  TYPE: PRIOR TITLING DATE: PRIOR DATE:	Query Match 100.0%; Score 1319; DB 10; Leng Best Local Similarity 100.0%; Pred. No. 9.9e-87; Matches 260; Conservative 0; Mismatches 0; Indel
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Query Match
Best Local Similarity
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APPLICANT: MCCARLIN, Seal A.

APPLICANT: Goodearl, Andrew D.J.

TITLE OF INVENTION: NOVEL GENES ENCODING PROTEINS HAVING

TITLE OF INVENTION: USES

CURRENT APPLICATION NUMBER: US/09/803,589

CURRENT APPLICATION NUMBER: US 09/128,709

PRIOR APPLICATION NUMBER: US 09/128,709

PRIOR APPLICATION NUMBER: US 09/128,709

PRIOR FILING DATE: 1998-08-04

PRIOR FILING DATE: 1997-08-06

PRIOR FILING DATE: 1997-09-06

PRIOR PLING DATE: 1997-09-05

PRIOR FILING DATE: 1997-09-01

PRIOR FILING DATE: 1997-09-01

PRIOR FILING DATE: 1997-09-01

PRIOR FILING DATE: 1999-09-01
                                                                                                                                 EEAGDETPDVDPELLRYLLGRILAGSADSEGVAAPRRLRRAADHDVGSELPPEGVLGALL 240
                                                                                                                                                                                                             61 RSVPRGEAAGAVQELARALAHLLEAERQERARAEAQEAEDQQARVLAQLLRVWGAPRNSD 120
                                                                                                           121 PALGLODDPDAPAAQLARALLRARLDPAALAAQLVPAPVPAAALRPRPPVYDDGPAGPDA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 RSVPRGEAAGAVQELARALAHLLEAERQERARAEAQEAEDQQARVLAQLLRVWGAPRNSD 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MAGSPLLWGPRAGGVGLLVLLLLGLFRPPPALCARPVKEPRGLSAASPPLAETGAPRRFR 60
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78.0%; Pred. No. 8.6e-38;
iive 6; Mismatches 27;
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SOCTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 14
LENCTH: 175
                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 14, Application US/09803589
Patent No. US20020112251A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                     241 RVKRLETPAPQVPARRLLPP 260
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Matches 131; Conservative
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US-09-803-589-14
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RESULT

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Sequence 190, Application us/0994271

Publication No. US200040088A1

GREERAL INFORMATION

TITLE OF INTENTION IN IMMAN SCREECE Proteins

TITLE OF INTENTION IN IMMAN SCREECE PROTEINS

TITLE OF INTENTION IN IMMAN SCREECE

CURRENT PRICE APPLICATION WURBER: 199/49.271

FRIOR FILING DATE: 1999-77.14

FRIOR FILING DATE: 1999-77.15

DATE: INCOMMATION: 1199

FRIOR FILING DATE: 1999-77.15

FRIOR FILING NAME: 1999-77.15

FRIOR FILING NAME: 1999-77.15

FRIOR FILING NAME: 1999-77.15

FROM FRIUNG FILING NAME: 1999-77.15

FROM FRIUNG FILING NAME: 1999-77.15

FROM FRIUNG NAME: 1999-77.15
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TYPE: PRT
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                                                                                                                                                                                                                                                     -----LR 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             111 RVWGAPRNSDPALGLDDDPDAPAQLARALLRARLDPAALAAQLVPAPVPAAALRPRPPV 170
                                                                                                                                                                                                            --APRRFRRSVPR-GEAAGAVQELARALAHLLEAERQERARAEAQEAEDQQARVLAQLLR 111
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                                                                                               Gaps
                                                                                                                                                   19 MAGSPELMGPRAGGVGLLVLLIGLFRPPPALCARPVKEPRGLSAASPPLARLALLAASG 78
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                                                                                                                                                                                                                                                                                       112 V----WGAPRNSDPALGLDDDPDAPAQLAR----ALLRARLDPAALAAQLVPA 157
                                                                                               50;
                                                                                                                                 1 MAGSPILWGPRAGGVGLLVLLLGLFRPPPALCARPVKEPRGLSAASPPLAETG---
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                                                      Score 308; DB 9; Length 166;
Pred. No. 3.6e-15;
3; Mismatches 34; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Steinthorsdottir, Valgerdur APPLICANT: Gulcher, Jeffrey R.
TITLE OF INVENTION: HUMAN SCHIZOPHRENIA GENE FILE REFERENCE: 2345.2004-001
CURRENT APPLICATION NUMBER: US/09/946,807
CURRENT APPLICATION NUMBER: US/09/795,668
PRIOR APPLICATION NUMBER: US/09/795,668
PRIOR PILING DATE: 2001-02-28
PRIOR FILING DATE: 2001-02-28
PRIOR FILING DATE: 2000-02-28
PRIOR FILING DATE: 2000-02-28
NUMBER OF SEQ ID NOS: 1531
SOFTWARE: FRASESO for Windows Version 4.0
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APPLICANT: Steinthorsdottir, Valgerdur
APPLICANT: Gulcher, Jeffrey R.
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; Sequence 3, Application US/09795668
; Patent No. US20020045577A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 3, Application US/09946807
Patent No. US2002015144A1
GENERAL INFORMATION:
APPLICANT: Stefansson, Hreinn
                                                      ch 23.4%;
il Similarity 50.3%;
88; Conservative
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WPTAPV-PSAGEPGEEAP 155
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; ORGANISM: Homo sapiens
US-09-984-271-238
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                                                      Query Match
Best Local S
Matches 88
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51 AETGAPRRFRRSVPRCEAAGAVQELARALAHLLEAERQERARAEAQEAEDQQARVLAQLL 110
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 3, Application US/09795686;
Patent No. US20020094954a1
GENERAL INFORMATION:
APPLICANT: Stefansson, Hreinn
APPLICANT: Stefanthorsdottir, Valgerdur
APPLICANT: Gulcher, Jeffrey R.
TITLE OF INVENTION: HUMAN SCHIZOPHRENIA GENE
FILE REFERENCE: 2345.2005-001
CURRENT APPLICATION NUMBER: US/09/795,686
CURRENT APPLICATION NUMBER: US/09/795,686
PRIOR RAPPLICATION NUMBER: US 09/515,715
PRIOR RILING DATE: 2000-02-28
NUMBER OF SEQ ID NOS: 1531
SOFTHARE: EastsEQ for Windows Version 4.0
; TITLE OF INVENTION: HUMAN SCHIZOPHRENIA GENE
; CURRENT APPLICATION NUMBER: US/09/795,668
; CURRENT FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: US 09/515,716
; PRIOR FILING DATE: 2000-02-28
; NUMBER OF SEQ ID NOS: 1531
; SOUTHARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; Score 124.5; DI
; Pred. No. 0.11;
14; Mismatches
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Best Local Similarity
Matches 57; Conserva
                                                                                                                                                                                                                                    LENGTH: 418
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US-09-795-668-3
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APPLICANT: Lees, Ann M.
APPLICANT: Lees, Robert S.
APPLICANT: Lay, Simon W.
TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING
TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING
TITLE OF INVENTION: ATHEOSCLEROSIS
PRIOR APPLICATION NUMBER: US/09/616,289
PRIOR FILING DATE: 2000-03-02
PRIOR FILING DATE: 2000-03-02
PRIOR FILING DATE: 1997-11.26
PRIOR APPLICATION NUMBER: US 60/031,930
PRIOR FILING DATE: 1996-11.26
PRIOR PELING DATE: 1996-11.27
PRIOR PELING DATE: 1996-11.27
PRIOR FILING DATE: 1996-11.27
PRIOR FILING DATE: 1996-11.27
PRIOR FILING DATE: 1996-11.27
PRIOR FILING DATE: 1997-06-03
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                    CURRENT APPLICATION NUMBER: US/10/023,529
CURRENT FILING DATE: 2001-12-17
PRIOR APPLICATION NUMBER: US/616,289
PRIOR FILING DATE: 2000-07-14
PRIOR FILING DATE: 2000-07-14
PRIOR FILING DATE: 2000-07-14
PRIOR FILING DATE: 1000-03-02
PRIOR FILING DATE: 1997-11-26
PRIOR FILING DATE: 1997-11-27
PRIOR FILING DATE: 1997-11-27
PRIOR FILING DATE: 1996-11-27
PRIOR FILING DATE: 1996-03
NUMBER OF SEQ ID NOS: 53
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 47
LENGTH: 550
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SOFTWARE: FastSEQ for Windows Version 4.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; TYPE: PRT
; ORGANISM: Oryctolagus cuniculus
US-10-023-529-47
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Matches 76; Conserv
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US-10-023-523-47
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APPLICANT: Lees, Robert S.
APPLICANT: Lees, Robert S.
APPLICANT: Lees, Robert S.
APPLICANT: Lewing M.
APPLICANT: Law, Simon W.
APPLICANT: Arjona, Anibal A.
TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING
TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING
TITLE OF INVENTION: ATHEROSCLEROSIS
TITLE OF INVENTION: ATHEROSCLEROSIS
CURRENT APPLICATION NUMBER: US/09/976,740
CURRENT FILING DATE: 2000-07-14
PRIOR APPLICATION NUMBER: 09/616,289
PRIOR FILING DATE: 1997-11-26
PRIOR APPLICATION NUMBER: US 60/031,930
PRIOR FILING DATE: 1997-11-27
PRIOR FILING DATE: 1996-11-27
PRIOR FILING DATE: 1996-11-27
PRIOR FILING DATE: 1996-11-27
PRIOR FILING DATE: 1997-60-03
NUMBER OF SEQ ID NOS: 53
SOFTWARE: FASLESEQ for Windows Version 4.0
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APPLICANT: Lees, Robert S.
APPLICANT: Law, Simon W.
APPLICANT: Law, Simon W.
APPLICANT: Arjons, Antbal A.
TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING
TITLE OF INVENTION: APOTEINS AND THEIR USE IN DIAGNOSING AND TREATING
TITLE OF INVENTION: ATHEROSCLEROSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10 PRAGGVGLLVLLLLGLFRPPPALCARPVKEPRG--LSAASP------PLAETGAP 56
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9.0%; Score 118.5; DB 9;
Best Local Similarity 28.4%; Pred. No. 0.39;
Matches 76; Conservative 14; Mismatches 103;
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                                                                                                                                                                                    Sequence 47, Application US/09976740 Publication No. US20020194633A1 GENERAL INFORMATION:
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Patent No. US20020129388A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; ORGANISM: Oryctolagus cuniculus US-09-976-740-47
171 YDDGPAGPDAEEAGDETP 188
                                                   139 WPTAPV-PSAGEPGEEAP 155
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                                                                                                                            203 -LAGSADSEGVAAPRRLRRAADHDVGSELPPEGVLG-ALLRVKRLETPAPQVPA 254
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                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE DOF INVENTION: NUCLEIC Acids, Proteins, and Antibodies
FILE REPERENCE: P2201
CURRENT APPLICATION NUMBER: US/09/764,898
CURRENT FILING DATE: 2001-01-17
Prior application data removed - consult PALM or file wrapper
NUMBER OF SEQ ID NOS: 311
SOFTWARE: Patentin Ver. 2.0
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TITLE OF INVENTION: 59079 and 12599, Protein Kinase Family
TITLE OF INVENTION: Members and USes Therefor
FILE REFERENCE: MF12001-047PIRCPI(M)
CURRENT APPLICATION NUMBER: US/10/077,130
CURRENT FILING DATE: 2002-02-15
PRIOR APPLICATION NUMBER: 60/269201
PRIOR APPLICATION NUMBER: 60/269201
NUMBER OF SEQ ID NOS: 9
                             160 PA-AALRPRPPVYDDGPAGPDAEEAGDETPDVDPELLRYLLGRI-
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Pred. No. 0.66;
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Patent No. US20020168742A1
GENERAL INFORMATION:
APPLICANT: Rapeller-Libermann, Rosana
APPLICANT: Acton, Susan L.
                                                                                                                                                                                                                                                                                           Sequence 206, Application US/09764898
Patent No. US20020090673A1
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Best Local Similarity 25.1%
Matches 78; Conservative
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US-09-764-898-206
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US-09-764-898-206
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APPLICANT: LEOPARDI, BERNARD
TITLE OF INVENTION: HERBES SIMPLEX VIRUS ICP4 IS AN INHIBITOR OF APOPTOSIS
FILE REPERBUCE: ARCD: 317USC1
CURRENT APPLICATION NUMBER: US/09/825,288A
CURRENT FILING DATE: 2001-04-02
PRIOR APPLICATION NUMBER: 09/259,821
PRIOR APPLICATION NUMBER: 08/690,473
PRIOR APPLICATION NUMBER: 08/690,473
PRIOR APPLICATION NUMBER: 08/690,473
PRIOR PILING DATE: 1996-07-26
SOFTWARE: PATENTIN VOS: 2.1
                                                                                                                                                                                                                                                                                   103 PRRGAT------PPA----PPRAPRGGPAAAAAPPTPAPPPPAPPAAAAAP 145
                                                                                                                                                                                                                                                                                                                                     57 RRFRRSVPRGEAAGAVQELARALAHLLEAERQERARAEAQEAEDQQARVLAQLLRVWGAP 116
                                                                                                                                                                                                                                                                                                                                                                                    146 AR----APRAAAAAAA----ATAPPSPGPAQPGPRA-----QRAAPLAAPPAPAAP 189
                                                                                                                                                                                                                                                                                                                                                                                                                                   117 RNSDPALGLDDDPDAPAAQLAR-ALLRARLDPAALAAQLVPAPVPAAALRPRPPVYDDGP 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                190 PAAAPPAGPRRAPPAAAVAARESPLPPPQPPAPPQQQQQPPPPPPPQQQQQPP----P 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               176 AGPDAEEAGDETPDVDPELLRYLLGRILAGSADSEG-----VAAPRRLRRAADHDV 226
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                                                                                                                                                  Length 550;
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                                                                                                                                             9.0%; Score 118.5; DB 12; Length ilarity 28.4%; Pred. No. 0.39; Conservative 14; Mismatches 103; Indels
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                                                 ; TYPE: PRT
; ORGANISM: Oryctolagus cuniculus
US-10-023-523-47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: HERPES VIRUS, TYPE 1
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Matches 88; Conservative
                                                                                                                                             Query Match
Best Local Similarity
Matches 76; Conserva
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SEQ ID NO 47
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                                                                                                                                                                       90;
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                                                                                                                                                                                                                                                                                -----QELARALAHLLEAERQERARAEAQEAEDQQARVLAQLLRVWG----
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                                                                                                                                 Query Match 8.5%; Score 112; DB 9; Length 2630; Best Local Similarity 27.7%; Pred. No. 6.4; Matches 81; Conservative 23; Mismatches 98; Indels 9
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Patent No. US20020168742A1
GENERAL INFORMATION:
APPLICANT: Kapellor-Libermann, Rosana
APPLICANT: Acton, Susan L.
TITLE OF INVENTION: 59079 and 12599, Protein Kinase Family
TITLE OF INVENTION: Members and Uses Therefor
FILE REFERENCE: MPIZ001-047PIRCP1(M)
CURRENT APPLICATION NUMBER: US/10/077,130
CURRENT FILING DATE: 2002-02-15
PRIOR APPLICATION NUMBER: 60/269201
PRIOR FILING DATE: 2001-02-15
NUMBER OF SEQ ID NOS: 9
SOFTWARE: FastSEQ for Windows Version 4.0
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SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 2
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                                                             TYPE: PRT
ORGANISM: Homo sapiens
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                                           LENGTH: 2630
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US-10-077-130-5
                                                                                               us-10-077-130-2
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APPLICANT: Lees, Robert S.
APPLICANT: Lees, Signon W.
TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING
TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING
TITLE OF INVENTION: ATHEROSCIEMOSIS
FILE REPERENCE: 10797-004001
CURRENT APPLICATION NUMBER: US/09/976,740
CURRENT FILING DATE: 2000-07-14
PRIOR APPLICATION NUMBER: US 08/979,608
PRIOR PELING DATE: 1997-11-26
PRIOR FILING DATE: 1997-06-03
PRIOR SED ID NOSER: US 60/031,930
PRIOR FILING DATE: 1997-06-03
NUMBER OF SED ID NOS: 53
SSOFTWARE: FESTSEQ for Windows Version 4.0
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LLRYLLGRILLAGSADSEGVAAPRRLRRAADHDVGSELPPE--GVLGALLRVK 243
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                                                                                                                                                                                    Sequence 43, Application US/09976740 Publication No. US20020194633A1 GENERAL INFORMATION:
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CAGANISM: Homo sapiens
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GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

April 4, 2003, 14:19:00; search time 74 Seconds (without alignments) 468.178 Million cell updates/sec

Run on:

US-09-803-589-6

Title: Perfect score:

260 1 MAGSPLLWGPRAGGVGLLVL.....RVKRLETPAPQVPARRLLPP 260 Sequence:

Scoring table:

OLIGO Gapop 60.0 , Gapext 60.0

908470 seqs, 133250620 residues Searched:

10 Word size :

14 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. /SIDS2/gcgdata/geneseg/genesegp-emb1/AA2000.DAT: /SIDS2/gcgdata/geneseg/genesegp-emb1/AA2001.DAT: /SIDS2/gcgdata/geneseg/genesegp-emb1/AA2002.DAT:

SUMMARIES

ption	acid sequenc	pituitary ho	polypeptide	hydrophobic	polypeptide	gene 48 enco	secreted pro	secreted pro	secreted pro	gene 48 enco
Description	Amino	Human	Human	Human	Human	Human	Нишаи	Нишап	Нишап	Human 9
A	AAW84597	AAY71959	AAM39005	AAB88596	AAM39006	AAE06088	ABG33910	AAY87111	AAY87199	AAE06176
DB	20	21	22	22	22	22	23	21	21	22
Query Match Length DB	260	260	260	260	223	148	148	149	166	166
Query Match	100.0	100.0	100.0	100.0	76.9	19.6	19.6	19.6	19.6	19.6
Score	260	260	260	260	200	51	51	51	51	21
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eted litar sequ						'n;									. s.		_	,		used to	are	cting		ıs, Tango		generate		; 0; Gaps
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						antibody; hybridisa									-81 p		0-81 p	ntain	gecific	in can or	ling a	ers fo	agnos	ingo p ints o	mapping and ozyme or	pe nsed		Length Indels
					protein										9 and associ		of the human Tango-81	. Host cells con	1fying	, wnic	c bind	prime hybrid	for di	Fragme	rit			DB 20; '.8e-213; ss 0;
	TS					protein ; primer									78, -7 rango-		human	ost ce	1dent	otors) In in	ecifi i frag	ses or	nsed	sston Jene.	genetic sense, rib	ss may		260; DB No. 7.8e natches
ABG34000 AAY71960 AAY71962 AAY71961	ALIGNMENTS	ė.			Tango	recombinant protein; gent; probe; primer; etic mapping.						SINC			ango-		f the	ntion. He	used in	recep	her sp ns and	s pro	s are	ango	used ror as antise	ibodi		🛏
ABG3 AAY7 AAY7 AAY7	AL	260 AA			human Tango-81	l; recomb g agent; genetic m						BIOTHERAPEUTICS			human Ta treatment	'n.	ence o	invention.	also us	cognate receptors), which can be binant protein in cells or	or ot	sed a	assay	the T	and as	3. Anț		Sc. Pr. 0;
23 21 21 21		in;		(¥.	the 1					241	645	IERAI			l tre	English.	edne	the in		e de la constant de l	lies int	be tally	lese.		e, Sp. 6	itics }.		100.0%; 100.0%; ive
166 258 262 69		, Protein;		t entry)	jo	<pre>go-81; host cell; specific binding .lon; mutation; ge</pre>				98WO-US16241	97US-0054645			3.	encoding human sis and treatme	67pp; Er	cic	of th	antibodies. It is	binding agents (including cognate receptors), which determine amounts of recombinant protein in cells or	therapeutically, Antibodies or other specific binding used to detect recombinant proteins and fragments of t	e can	ys. Th	ations	d sequence are also used for gene identification, and as antisense,	ng therapeut antibodies.		100 larity 100 Conservative
9.7.7.9		ırd;		(first	enc	fic				98W	970	MOI		3/1	d e			method	lies	ts	rec	sp	155a	Mut	ᅜᆛ	G	AA;	ity
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51 33 12		•	97;	03-JUN-1999	acid	Tan Tan Cat	sapiens	427-A1	-FEB-1999	04-AUG-1998	-AUG-1997		hy SA;	999-153693/13 ; AAV68668.	New nucleic useful for d	1; Fig		늄		g age ine a	eutic o det	tide ngo g	icati	etect	acı one	triplex-forming anti-idiotype a	g G	ch 1 Sim 260;
		T 1 597 AAW84597	AAW84597	- JUN	Amino	Human; receptc amplifi	Ното в	WO9906427	-FEB	-AUG	-AUG	(MILL-)	McCarthy	WPI; 19 N-PSDB;	w nu eful	Claim	This 1		raising	oinaing determi	erap	cleor e Ta	plif	9 c	romo	triplex anti-id	Sequence	atca
11 12 14		RESULT 1 AAW84597 ID AAW8	A	03	Ā	Hu re	HO	M	11	04	04	Ξ	MC	W.	Ne	ე.	Th	use + ho	i d	ge 5	th us	감	am	j 0	당	tr an	Se	Query M Best Lo Matches
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useful

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The present sequence is a human pituitary hormone, pituitrone (clone HKGDL36). Pituitrone is highly expressed in pituitary or gland and is also expressed in brain tissues, spinal cord and kidney. It may be used as antigens in the production of antibodies against pituitrone and in assays to identify modulators. Pituitrone cDNAs are also useful in gene therapy. Pituitrone may be used in the prevention, treatment and diagnosis of diseases associated with inappropriate pituitrone expression. It may be useful in treating disorders related to reproductive and renal system, immune disorders, disorders of haematopoietic cells (e.g., anaemia, Digeorge syndrome, ataxia telangiectasia and Wiskott-Aldrich disorder), blood coagulation disorders, autoimmune disorders (e.g. Addison's disease, multiple sclerosis and systemic lupus errythematosus (SLE)), hyperproliferative disorders (e.g. neoplasms of bone, liver and pancreas) and infectious
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer; peripheral nervous system; neuropathy; central nervous system; CNS; Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic; amyotrophic lateral scleroslis; Shy-brager Syndrome; chemotactic; chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 RSVPRGEAAGAVQELARALAHLLEAERQERARAEAQEAEDQQARVLAQLLRVWGAPRNSD 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MAGSPLLWGPRAGGVGLLVLLLLGLFRPPPALCARPVKEPRGLSAASPPLAETGAPRFFR 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nucleic acids encoding a novel pituitary hormone (pituitrone), for diagnosing, preventing and treating e.g. immune disorders, hyperproliferative disorders and blood coagulation disorders -
                                                                                                                                                                                                                                                                                                                                                        Score 260; DB 21;
Pred. No. 7.8e-213;
0; Mismatches 0;
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                                                                                    Claim 11; Fig 1; 277pp; English.
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nes 260; Conservative
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    N-PSDB; AAD02075.
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EEAGDETPDVDPELLRYLLGRILAGSADSEGVAAPRRLRRAADHDVGSELPPEGVLGALL
                                                     PALGLDDDPDAPAAQLARALLRARLDPAALAAQLVPAPVPAAALRPRPPVYDDGPAGPDA
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/label- Signal_peptide
34..260
/label- Mature_human_pituitrone
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/note= "Highly immunogenic"
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Length 260; Indels 9

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Human; hydrophobic domain; immunosuppressant; anti-HIV; neuroprotective; antianaemic; vulnerary; antiulcer; osteopathic; anti-inflammatory; cytostatic; gene therapy; autoimmune disorder; multiple sclerosis; HIV infection; anaemia; burn; ulcer; osteoporosis; tumour; wound healing; inflammatory bowel disease; nutritional supplement; appetite; vaccine; behavioural characteristic; immune response.
                                                            Human hydrophobic domain containing protein clone HP10756 #100.
                                                                                                                                                                                                                                     10-AUG-2000; 2000WO-JP05356
                                    04-JUN-2001 (first entry)
                                                                                                                                                                                        WO200112660-A2.
                                                                                                                                                                                                                                                                                                                                  SAGA ) SAGAMI
                                                                                                                                                                   Homo sapiens,
                                                                                                                                                                                                              22-FEB-2001
                                                                                                                                                                                                                                                              17-AUG-1999
                                                                                                                                                                                                                                                                         07-SEP-1999
                                                                                                                                                                                                                                                                                                22-OCT-1999
04-NOV-1999
                                                                                                                                                                                                                                                                                      01-0CT-1999
              AAB88596;
                                                                                                                                                                                                                                                                                                                                               (PROT-)
  The invention relates to human nucleic acids (AAIS7798-AAI61369) and the encoded polypeptides (AAM38642-AAM42213) with nootropic, farminosouppressant and cytostatic activity. The polynucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral neuropathy and localised neuropathles and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the Activities such as: Immune system suppression, Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, arthritis and inflammation, leukaemias and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The sequence data for this patent did not form part of the printed
                                                                                                                                                                  Wang D;
                                                                                                                                                                                                                                               Novel nucleic acids and polypeptides, useful for treating disorders such as central nervous system injuries -
                                                                                                                                                                Ren F, W
Zhang J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 260;
                                                                                                                                                                Qian XB,
Yang Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 260; DB 22; 100.0%; Pred. No. 7.8e-213;
                                                                                                                                                               ten R, Ma Y, C
Ku C, Xue AJ,
Drmanac RT;
                                                                                                                                                                                                                                                                                   Example 4; SEQ ID NO 2150; 10078pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
                                                                                                                                                               Chen R,
                                                                                                                                                                           Xu C,
                                                                                                                                                              Asundi V, Che
Wehrman T, Xu
Goodrich R,
                                                                                          2000US-0662191.
2000US-0693036.
           26-DEC-2000; 2000WO-US34263
                                                         2000US-0598042
                                                                    2000US-0620312.
2000US-0653450.
                                                                                                                  2000US-0727344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches 260; Conservative
                                                                                                                                                                                                              WPI; 2001-442253/47
                                                                                                                                                              Liu C, A
Wang Z, V
Zhou P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity
                                                                                                                                         (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            260 AA;
                                                                                                                                                                                                                         N-PSDB; AAI58161
                                                                                                                                                                                                                                                                                                                                                                                                                                                  assays for recel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   specification.
                                                                                          14-SEP-2000;
19-OCT-2000;
29-NOV-2000;
                                                                    19-JUL-2000;
                                                                                 03-AUG-2000;
                                             25-APR-2000;
                                                                                                                                                                           Wang J, 1
Zhao QA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                               Tang YT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
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CHEM RES CENT

PROTEGENE INC.

99JP-0252551.

99JP-0301624 99JP-0313877

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                                                                                     PALGLDDDPDAPAAQLARALLRARLDPAALAAQLVPAPVPAAALRPRPPVYDDGPAGPDA 180
                                                                                                                                                                        EEAGDETPDVDPELLRYLLGRILAGSADSEGVAAPRRLRRAADHDVGSELPPEGVLGALL 240
                                                                        RSVPRGEAAGAVQELARALAHLLEAERQERARAEAQEAEDQQARVLAQLLRVWGAPRNSD 120
   Gaps
                                      1 MAGSPLLWGPRAGGVGLLVLLLLGLFRPPPALCARPVKEPRGLSAASPPLAETGAPRRFR 60
  ö
0; Indels
                                                                                                                                                                                                                         RVKRLETPAPQVPARRLLPP 260
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ò g ð g AAB88596 standard; Protein; 260 AA.

RESULT 4 AAB88596 ID AAB8

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AABBBB60 (I) which have a hydrophobic domain. (I) have immunosuppressant, anti-flay, neuroprotective, anti-flame and vulnerary, anti-floss.

Ca AABBB606 (I) which have a hydrophobic domain. (I) have immunosuppressant, corepopting. In the case of the cativities, and can be used an anti-flammatory and cytostatic activities, and can be used in gene therapy. (I) can be used as pharmaceuticals and as antigens of probes for genetic diagnosis and gene sources for gene therapy or for producing (I) in large quantities. Cells containing (II) are used for the detection of ligands or receptors corresponding to membrane or secretory proteins and to screen small molecule novel pharmaceuticals.

Cantibodies directed to (I) can be used for the detection, quantification and purification of (I). Activities of (I) may include cytokine and cell proliferation/differentiation function, immune stimulating or suppressing activity, haematopolesis regulating activity, tissue growth activity, activity, chemotactic/chemokinetic activity, haemacory cativity, chemotactic/chemokinetic activity, haemacory cativity, and (II) can be used to treat autoimmune disorders e.g. multiple sclerosis, HIV infections, anaemia, burns, ulcers, osteoporosis, contained the contained c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            wound healing, as nutritional sources or supplements e.g. as amino acid, carbon or nitrogen source, to effect metabolism, catabolism, anabolism, processing and utilisation of dietary fat, protein, carbohydrate,
                                                                                                                                                                                                                                                                                                              Human proteins with hydrophobic domains and the DNAs which encode them are useful for treating autoimmune disorders, burns and tumors and for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; Page 422-423; 518pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                        screening novel pharmaceuticals -
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Matches 260; Conservative
                                                                                                                   WPI; 2001-160059/16.
Kato S, Kimura T;
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                                                                                                                                                                                          N-PSDB; AAF94486
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13-JAN-2000; 2000US-0482273
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         19-JUL-2001
                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                          AAE06088;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Protein
                                                                                                                                                                                                                                                                                                             181
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                                                                                                                                                                                                                                                                                        Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer; peripheral nervous system; neuropathy; central nervous system; CNS; Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic; amyotrophic lateral scleroals; SNy-Drager Syndrome; chemotractic; chemotractic; thrombolytic; drug screening; arthritis; inflammation;
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                                                                                                                 EEAGDETPDVDPELLRYLLGRILAGSADSEGVAAPRRLRRAADHDVGSELPPEGVLGALL 240
                                                                                                                          RSVPRGEAAGAVQELARALAHLLEAERQERARAEAQEAEDQQARVLAQLLRVWGAPRNSD 120
                                                                             PALGLDDDPDAPAAQLARALLRARLDPAALAAQLVPAPVPAAALRPRPPVYDDGPAGPDA 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Wang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel nucleic acids and polypeptides, useful for treating disorders such as central nervous system injuries -
                MAGSPLLWGPRAGGVGLLVLLLLGLFRPPPALCARPVKEPRGLSAASPPLAETGAPRRFR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ren F, W
Zhang J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Otan XB,
Yang Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Liu C, Asundi V, Chen R, Ma Y,
Wang Z, Wehrman T, Xu C, Xue AJ,
Zhou P, Goodrich R, Drmanac RT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 4; SEQ ID NO 2151; 10078pp; English.
                                                                                                                                                                                                                  AAM39006 standard; Protein; 223 AA.
                                                                                                                                                                                                                                                                        Human polypeptide SEQ ID NO 2151.
                                                                                                                                                     RVKRLETPAPQVPARRLLPP 260
                                                                                                                                                             2000US-0653450.
2000US-0662191.
2000US-0693036.
                                                                                                                                                                                                                                                                                                                                                                                                                             2000US-048B725.
2000US-0552317.
2000US-0598042.
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14-SEP-2000; 2000US-0662191
19-OCT-2000; 2000US-0693036
29-NOV-2000; 2000US-0727344
                                                                                                                                                                                                                                                      (first entry)
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N-PSDB; AAI58162.
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                                                                                                                                                                                                                                                                                                                                                       Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                              21-JAN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                        25-APR-2000;
09-JUL-2000;
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                                                                                                                                                                                                                                                      22-OCT-2001
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В,
                                                                                                                                                                                                                                                                                                                                      leukaemia
                                                                                                                                                                                                                                   AAM39006;
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                                                                                                                                                                      241
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in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral nervous system, such as peripheral nervous injuries, peripheral nervous system diseases, such as alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activities such as: Immune system suppression, Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, cancer disgnosis and therapy, drug screening, assays for receptor activity, arthritis and inflammation, leukaemias and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; secreted protein; proliferative disorder; cancer; tumour; asthma; foetal abnormality; developmental abnormality; haematopoietic disorder; lumnune system disorder; AIDS; autoimmune disease; rheumatoid arthritis; Parkinson's disease; cognitive disorder; schizophrenia; skin disorder; psoriasis; sepsis, diabetes; atherosclerosis; cardiovascular disorder; inflammation; neurological disorder; Alzhelmer's disease; food additive; anglogenic disorder; Kidney disorder; gastrointestinal disorder; allergy; pregnancy-related disorder; endocrine disorder; infection; wound healing; gene therapy.
                                                                                                                                                                                                                                                                                                                       C.N.S disorders.

Note: The sequence data for this patent did not form part of the printed specification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 RSVPRGEAAGAVQELARALAHLLEAERQERARAEAQEAEDQQARVLAQLLRVWGAPRNSD 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121 PALGLDDDPDAPAAQLARALLRARLDPAALAAQLVPAPVPAAALRPRPPVYDDGPAGPDA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MAGSPLLWGPRAGGVGLLVLLLLGLFRPPPALCARPVKEPRGLSAASPPLAETGAPRRFR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human gene 48 encoded secreted protein HKGDL36, SEQ ID NO:150.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 223;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
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/label= Mature_human_secreted_protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6.7e-162;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 76.9%; Score 200; DE 100.0%; Pred. No. 6.7 ive 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAE06088 standard; Protein; 148 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches 200; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                        223 AA;
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Best Loca
Matches
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à
                                                                                                                                                                                                                                                                                                                                                                     AAD11630-AAD11721 represent CDNAs corresponding to 71 human secreted
protein genes, and AAE06041-AAE06132 represent the proteins they encode.

CC AAE06133-AAE06205 represent human secreted protein fragments.

CT AAE06133-AAE06205 represent human secreted protein fragments.

CT has secreted proteins and their genes are useful for preventing, treating

CC or ameliorating medical conditions, e.g., by protein or gene therapy.

CC Pathological conditions can be diagnosed by determining the amount of the

CC new protein in a sample or by determining the presence of mutations in

CC the new genes. Specific uses are described for each of the 71 genes,

CC based on the tissues in which they are most highly expressed, and include

CC developing products for the diagnosis or treatment of proliferative

CC disorders, cancer, tumours, foetal and developmental abnormalities,

CC haematopoietic disorders, diseases of the immune system, AIDS, autoimmune

CC diseases (e.g., rheumatoid arthritis), inflammation, allergies,

CC diseases (e.g., Alzheimer's disease, Parkinson's disease),

CC diseases (e.g., Alzheimer's disease, Parkinson's disease),

CC ognitive disorders, schizophrenia, asthma, skin disorders,

CC proteins can also be used to aid wound healing and epithelial cell

CC proteins can also be used to aid wound healing and epithelial cell

CC proteins can also be used to aid wound healing and epithelial consumpration, to prevent skin aging due to sunburn, to maintain organs

CD perferation, to prevent skin aging due to sunburn, to maintain organs

CD perfere transplantation, for supporting cell culture of primary tissues,

CD perferences, and in chemotrais, and can be used as a food additive for an and and an expension and additive for an analysis and can be used as a food additive for an expension and an expension and additive for an analysis and can be used as a food additive for an expension and additive for an expension and additive for an expension 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                preservative to modify storage properties. Antibodies specific for a protein of the invention can be used in alleviating symptoms associated with the disorders mentioned above, and in diagnostic immunoassays e.g., radioimmunoassay or enzyme linked immunosorbent assay (ELISA). The present sequence represents a human secreted protein of
                                                                      Shi Y;
Soppet DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                   Isolated nucleic acid molecule encoding a human secreted protein is used in preventing, treating or ameliorating a medical condition
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                         Moore PA,
Young PE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   19.6%; Score 51; DB 22; Length 148; 100.0%; Pred. No. 2e-35; 1ve 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MAGSPLLWGPRAGGVGLLVLLLLGLFRPPPALCARPVKEPRGLSAASPPLA 51
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                                                                   Duan DR, Rosen CA, I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Pred. no.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human secreted protein encode by gene 48.
                                                                                                                                                                                                                                                                                                                               Claim 11; Page 773-774; 864pp; English.
                                                              Ruben SM, Komatsoulis GA, Duan DR
Lafleur DW, Olsen HS, Brewer LA,
Endress GA, Muscenski M, Ebner R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABG33910 standard; Protein; 148 AA.
                  (HUMA-) HUMAN GENOME SCI INC.
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                                                                                                                                                                  WPI; 2001-425865/45.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     148 AA;
                                                                                                                                                                                                N-PSDB; AAD11677
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15-JUL-2002
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Matches
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The invention relates to an isolated nucleic acid molecule (or its fragment, homologue complement or allelic variant) encoding a human secreted protein (and its fragment, domain, epitope, variant, secreted form and species variant). Also included are a recombinant vector comprising the nucleic acid, a recombinant host cell comprising the nucleic acid, a recombinant host cell that expresses the secreted protein, a recombinant host cell that expresses the secreted protein and a method of identifying a binding partner of the secreted protein. The nucleic acid and protein are used to prevent, diagnose, treat or amelicante a medical condition in e.g. humans, mice, rabbits, goats, horses, cats, dogs, chickens or sheep for example autoimmune diseases e.g. rheumatoid arthritis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          skin aging due to sunburn, to maintain organs before transplantation, for supporting cell culture of primary tissues, to regenerate tissues and in chemotaxis. The polypeptides can also be used as a food additive or preservative to increase or decrease storage capabilities. The present sequence represents a novel human secreted protein of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  hyperproliferative disorders e.g. neoplasms of the breast or liver, cardiovascular disorders e.g. cardiac arrest, cerebrovascular disorders e.g. cerebral ischaemia, anglogenesis, nervous system disorders e.g. Alzheimer's disease, infections caused by bacteria, viruses and fungi and ocular disorders e.g. corneal infection. Many other diseases and disorders are listed in the specification. The polypeptides can also be used to aid wound healing an epithelial cell proliferation, to prevent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel 71 isolated secreted polypeptides and polynucleotides encoding the polypeptides, useful for treating Huntington's disease, sepsis, meningitis, thrombocytopaenia, haemolytic anaemia, rheumatoid arthritis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Soppet DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Shi Y;
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ocular disorder; corneal infection; wound healing; skin aging; epithelial cell proliferation; food additive.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Moore PA,
Young PE,
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Florence KA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 11; Page 1252-1253; 1478pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Komatsoulis G, Duan DR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Brewer LA,
f, Ebner R;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                                                                                                                                                                                                                                                                              25-SEP-2000; 2000US-234925P.
12-JAN-2001; 2001WO-US00911.
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Endress GA, Mucenski M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2002-362489/39.
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Les 51; Conserv
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                                                                                                                                                                                 WO200226931-A2
                                                                                                              Homo sapiens.
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                                                                                                                                                                                                                                                            04-APR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ruben SM,
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antinflammatory; notropic; neuroprotective; antiallergic; cancer; antinflammatory; notropic; neuroprotective; antiallergic; cancer; tumour; neurodegenerative disorder; developmental abnormality; allergy; foetal deficiency; blood disorder; immune system disorder; architits; autoimmune disease; hepatic disease; renal disease; inflammation; Albaiener; s disease; behavioural disorder; schizophrenia; osteoporosis; infection; AlbS; spinal cord injury; transplant rejection; diabetes; asthma; sepsis; acne; psoriasis; cardiovascular disorder; reproductive disorder; gastrointestinal disorder; respiratory disorder; metabolic disorder; food additive; preservative.

Human secreted protein sequence SEQ ID NO:238.

(first entry)

09-MAY-2000

AAY87199;

AAY87199 standard; Protein; 166 AA.

RESULT 9 AAY87199

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The polynucleotide sequences given in AAY98017 to AAX98108 encode the human secreted proteins given in AAY87064 to AAX8723. Human secreted proteins given in AAY87064 to AAX8723. Human secreted protein can have activities based on the tissues and cells the genes are expressed in Examples of activities include: cytostatic; immunosuppressive; antiinflammatory; nootropic; neuroprotective; and antialergic. The polynucleotides and their corresponding secreted polypeptides are useful for preventing, treating or ameliorating medical conditions, e.g. by protein or gene therapy. Also pathological conditions can be diagnosed by determining the amount of the new polypeptides in a sample or by determining the presence of mutations in the new polypeptides can be used for developing products for the diagnosis or treatment of cancer, tumours, neurodegenerative disorders, developmental abnormalities and focatal deficiencies, blood disorders, diseases of the immune system, allocation of the control 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               preservatives. The proteins are also useful for identifying their binding partners. AAZ98008 to AAZ98016 and AAY87063 are sequence used in the exemplification of the present invention.
                                                                                  antinflammatory; nootropic; neuroprotective; antiallergic; cancer; tumour; neurodegenerative disorder; developmental abnormality; allergy; foetal deficiency; blood disorder; developmental abnormality; allergy; autoimmune disease; inclammation; alzheimer's disease; hepatic disease; renal disease; inflammation; Alzheimer's disease; behavioural disorder; schizophrenia; osteoporosis; infection; AlDS; spinal cord injury; transplant rejection; diabetes; asthma; sepsis; acne; psoriasis; cardiovascular disorder; disorder; respiratory disorder; metabolic disorder; food additive; preservative.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Shi Y;
Young PE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       allergies, Alzheimer's disease, behavioural disorders, schizophrenia, osteoporosis, arthritis, infections, AIDS, spinal cord injuries,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New isolated human genes, useful for diagnosis and treatment of, e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           transplant rejection, diabetes, asthma, sepsis, acre, psoriasis, cardiovascular disorders, reproductive disorders, gastrointestinal disorders, respiratory disorders and metabolic disorders. The proteins or polynucleotides can also be used as food additives or preservatives. The proteins or perservatives are also useful for identifying their
                                                          Human; secreted protein; diagnosis; cytostatic; immunosuppressive;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Duan RD, Rosen CA, Moore PA,
en HS, Brewer LA, Florence KA,
   Human secreted protein sequence SEQ ID NO:150.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cancers, neurological or blood disorders
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A, Soppet DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (HUMA-) HUMAN GENOME SCI INC
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98US-0092956.
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Endress GA,
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                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens.
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Young PE;

G, Duan RD, Rosen CA, Moore PA, Olsen HS, Brewer LA, Florence KA, \(\text{\chi}\), Soppet DR;

(HUMA-) HUMAN GENOME SCI INC.

15-JUL-1998; 15-JUL-1998;

Komatsoulis G, Ebner R, Ol Endress GA,

Lafleur DW, Mucenski M,

Ruben SM,

WPI; 2000-161128/14. N-PSDB; AAZ98064.

99WO-US15849. 98US-0092921. 98US-0092922 98US-0092956

14-JUL-1999; S-JUL-1998;

27-JAN-2000.

WO200004140-A1. Homo sapiens.

Shi Y;

New isolated human genes, useful for diagnosis and treatment of, e.g.

cancers, neurological or blood disorders Disclosure; Page 470; 494pp; English.

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antiallergic. The polynucleotides and their corresponding secreted antiallergic. The polynucleotides and their corresponding secreted antiallergic. The polynucleotides and their corresponding secreted polypeptides are useful for preventing, treating or ameliorating medical conditions, e.g. by protein or gene therapy. Also pathological conditions can be diagnosed by determining the amount of the new polypeptides in a sample or by determining the presence of mutations in the new polypeptides in a polymucleotides. Bunam secreted protein s and their polymucleotides can be used for developing products for the diagnosis or treatment of cancer, tumours, neurodegenerative disorders, developmental abnormalities and foetal deficiencies, blood disorders, diseases of the immune system, autoimmune diseases, hepatic and renal disease, inflammation, allergies, Alzheinmer's disease, behavioural disorders, solizophrenia, osteoporosis, arthritis, infections, AlDS, spinal cord injuries, transpant rejection, diabetes, asthma, sepsis, acne, psoriasis, cardiovascular disorders and metabolic disorders. The proteins or polynucleotides can also be used as food additives or proteins or polynucleotides can also be used as food additives or proteins are also useful for identifying their binding partners. AAZ38008 to AAZ38006 and AAX87063 are sequence used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             human secreted proteins given in AAY87064 to AAY87223. Human secreted protein can have activities based on the tissues and cells the genes are expressed in. Examples of activities include: cytostatic;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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Query Match
Best Local Similarity 100.(
Matches 51; Conservative

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Lafleur
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ABG34000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The secreted proteins and their genes are useful for preventing, treating or ameliorating medical conditions, e.g., by protein or gene therapy.
The stablogical conditions can be diagnosed by determining the amount of the new protein in a sample or by determining the presence of mutations in the new genes. Specific uses are described for each of the 71 genes, based on the tissues in which they are most highly expressed, and include developing products for the diagnosis or treatment of proliferative disorders, cancer, tumours, foetal and developmental abnormalities, haematopoietic disorders, diseases of the immune system, AIDS, autoimmune fliesases (e.g., rheumatoid arthritis), inflammation, allergies, neurological disorders, schizophrenia, asthma, skin disorders (e.g., psoriasis), sepsis, diabetes, atherosclerosis, cardiovascular disorders, angiogenic disorders, tidney disorders, gastrointestinal disorders, angiogenic disorders, schizophrenia, asthma, skin disorders, angiogenic disorders, tidney disorders, gastrointestinal disorders,
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                                                                                                                                                                                                                                                                                                                                                                                                                                        foetal abnormality; developmental abnormality; haematopoletic disorder; immune system disorder; ALDS; autoimmune disease; rheumatoid arthritis; Parkinson's disease; cognitive disorder; schizophrenia; skin disorder; psoriasis; sepsis; diabetes; atherosclerosis; cardiovascular disorder; inflammation; neurological disorder; Alzheimer's disease; food additive; anglogenic disorder; kindney disorder; askrointestinal disorder; allergy; pregnancy-related disorder; endocrine disorder; allergy; cell culture; chemotaxis; vulnerary; binding partner identification;
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AAE06133-AAE06205 represent human secreted protein fragments.
                                                                                                                                                                                                                                                                                                                                                                                                                        secreted protein; proliferative disorder; cancer; tumour; asthma;
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Soppet DR;
                                                                                            Gaps
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Young PE,
                                                                                                                                                19 MAGSPLLMGPRAGGVGLLVLLLLGLFRPPPALCARPVKEPRGLSAASPPLA 69
                                                                                                                                1 MAGSPLLWGPRAGGVGLLVLLLLGLFRPPPALCARPVKEPRGLSAASPPLA 51
                                  DB 21; Lens
0. 2.2e-35; Indels
                                                      Length 166;
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                                            19.6%; Score ...
100.0%; Pred. No. 2.2e-
-**** 0; Mismatches
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                                                                                                                                                                                                                                                                AAE06176 standard; Protein; 166 AA
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Olsen HS, Bre
Muscenski M,
                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                            51; Conservative
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                                                                        Similarity
                166 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                gene therapy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Lafleur DW,
Endress GA,
                                                                                                                                                                                                                                                                                                      AAE06176;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    S,
                Sequence
                                                      Query Match
                                                                          Local
                                                                                                                                                                                                                                                                                                                                                                                                                        Human;
                                                                                          Matches
                                                                                                                                                                                                                              RESULT 10
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pregnancy-related disorders, endocrine disorders, and infections. The proteins can also be used to aid wound healing and epithelial cell proliferation, to prevent skin aging due to sunburn, to maintain organs before transplantation, for supporting cell culture of primary tissues, to regenerate tissues, to identify their cognate ligands or binding partners, and in chemotraxis, and can be used as a food additive or preservative to modify storage properties. Antibodies specific for a protein of the invention can be used in alleviating symptoms associated with the disorders mentioned above, and in diagnostic immunoassay or enzyme linked immunosochent assay (ELISA).

The present sequence represents a human secreted protein fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel 71 isolated secreted polypeptides and polynucleotides encoding the polypeptides, useful for treating Huntington's disease, sepsis, meningitis, thrombocytopaenia, haemolytic anaemia, rheumatoid arthritis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Shi Y;
Soppet DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to an isolated nucleic acid molecule (or its fragment, homologue complement or allelic variant) encoding a human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MAGSPLIWGPRAGGVGLLVLLLGLFRPPPALCARPVKEPRGLSAASPPLA 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       19 MAGSPLLWGPRAGGVGLLVLLLGLFRPPPALCARPVKEPRGLSAASPPLA 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 51; DB 22; Length 166;
Pred. No. 2.2e-35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Moore PA,
Young PE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; secreted protein; gene therapy; immunosuppressive;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   , Rosen CA, I
Florence KA,
                                                                                                                                                                                                                                                                                                                                                                                            referred to in the disclosure of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human secreted protein #2 encoded by gene 48.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                19.6%; Sco. 100.0%; Pred. No. ... 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Page 1316-1317; 1478pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Duan DR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABG34000 standard; Protein; 166 AA.
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Olsen H, Brewer LA,
Mucenski M, Ebner R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (HUMA-) HUMAN GENOME SCI INC.
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12-JAN-2001; 2001WO-US00911.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     24-SEP-2001; 2001WO-US29871.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15-JUL-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                51; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2002-362489/39.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            166 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N-PSDB; ABK69773
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     04-APR-2002.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
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Best Local
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(HUMA-) HUMAN GENOME SCI INC.

N1 J;

Ruben SM,

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Secreted protein (and its ladguent, commain, epilope, variant, secreted form and species variant). Also included are a recombinant vector comprising the nucleic acid, a recombinant host cell comprising the nucleic acid, a recombinant host cell comprising the nucleic acid, a recombinant host cell that expresses the secreted protein and method of identifying a binding partner of the secreted protein. The nucleic acid and protein are used to prevent, diagnose, treat or ameliorate a medical condition in e.g. or ambalis, goats, horses, cats, dogs, chickens or sheep for example autoimmune diseases e.g. rheumatoid arthritis, hyperproliferative disorders e.g. rheumatoid arthritis, cardiovascular disorders e.g. rheumatoid arthritis, cardiovascular disorders e.g. cardiac arrest, cerebroascular disorders e.g. cardiac arrest, cerebroascular disorders e.g. cardiac arrest, cerebroascular disorders e.g. cardiac arrest, or symboritar disorders e.g. corneal infection. Many other diseases and disorders are listed in the specification. The polypeptides can also be used at oaid wound healing an epithalal cell proliferation, to prevent supporting call culture of primary tissues, to regenerate tissues and in chemotaxis. The polypeptides can also be used as a food additive or preservative to increase or decrease storage capabilities. The present corrected protein of the invention.
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   domain, epitope, variant, secreted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /label- Signal_peptide
/note- "An alternative signal sequence referred in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note= "Mature mouse pituitrone" | Amature mature protein referred in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mouse; pituitary; pituitrone; therapy; immune disorder; anaemia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             69
                                                                                                                                                                                                                                                                                                                                                                                                                                              19 MAGSPLLWGPRAGGVGLLVLLLGLFRPPPALCARPVKEPRGLSAASPPLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MAGSPLLWGPRAGGVGLLVLLLLGLFRPPPALCARPVKEPRGLSAASPPLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Mature mouse pituitrone"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /label= Signal_peptide
35..258
protein (and its fragment, species variant). Also incl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mouse pituitary hormone, pituitrone.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAY71960 standard; Protein; 258 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    19.68;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            26-MAR-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similaricy -
nes 51; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   page 11"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             page 11"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note-
                                                                                                                                                                                                                                                                                                                                                                                                               166 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30-APR-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus sp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
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                                                                                                                                                                                                                          The present sequence is a mouse pituitary hormone, pituitrone. Pituitrone is highly expressed in pituitary gland and is also expressed in brain tissues, spinal cord and kidney. It may be used as antigens in the production of antibodies against pituitrone and in assays to identify modulators. Pituitrone cDNAs are also useful in gene therapy. Pituitrone may be used in the prevention, treatment and diagnosis of diseases associated with inappropriate pituitrone expression. It may be useful in treating disorders related to reproductive and renal system, immune disorders, disorders of
                                                                                                                                 useful
                                                                                                                                                                                                                                                                                                                                                                                                              disorders, autoimmune disorders (e.g. Addison's disease, multiple sclerosis and systemic lupus erythematosus (SLE)), hyperproliferative disorders (e.g. neoplasms of bone, liver and pancreas) and infectious
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                             haematopoietic cells (e.g., anaemia, Digeorge syndrome, ataxia telangiectasia and Wiskott-Aldrich disorder), blood coagulation
                                                                                                                             Nucleic acids encoding a novel pituitary hormone (pituitrone), for diagnosing, preventing and treating e.g. immune disorders, hyperproliferative disorders and blood coagulation disorders -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 258;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Consensus sequence of human, mouse and rat pituitrone.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Pred. No. 6.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               126 DDDPDAPAQLARALLRARLDPAALAAQLVPAP 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12.7%; Score 33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
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                                                                                                                                                                                               Claim 11; Fig 2; 277pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAY71962 standard; Protein; 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 label- Unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  'label - Unknown
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 12.73
Best Local Similarity 100.
Matches 33; Conservative
                                                                           WPI; 2000-687547/67
N-PSDB; AAD02076.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 258 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Misc-difference 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Misc-difference 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Misc-difference
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 13
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The present sequence is a consensus sequence of human, mouse and rate pitulitrone. Pitulitrone is highly expressed in pitulitary gland and is also expressed in brain tissues, spinal cord and kidney. Pitulitrone may be used as antigens in the production of antibodies against cord pitulitrone and in assays to identify modulators. Pitulitrone cDNAs are also useful in gene therapy. Pitulitrone may be used in the prevention, treatment and diagnosis of diseases associated with inappropriate treatment and diagnosis of diseases associated with inappropriate to pitulitrone expression. It may be useful in treating disorders related to reproductive and renal system, immune disorders, disorders of hematopoietic cells (e.g., anaemia, Digeorge syndrome, ataxia telangiectasia and Wiskott-Aldrich disorder), blood coagulation classical and systemic lupus erythematosus (SLE), hyperproliferative disorders (e.g. neoplasms of bone, liver and pancreas) and infectious
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Digeorge syndrome; haematopoietic cell; ataxia telangiectasia; Digeorge syndrome; haematopoietic cell; ataxia telangiectasia; Wiskott-Aldrich disorder; blood coagulation disorder; Addison's diseas autoimmune disorder; multiple sclerosis; systemic lupus erythematosus;
                                                                                                                                                                                                             Nucleic acids encoding a novel pituitary hormone (pituitrone), useful for diagnosing, preventing and treating e.g. immune disorders, hyperproliferative disorders and blood coagulation disorders -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SLE; hyperproliferative disorder; gene therapy; neoplasm;
infectious disease; immunomodulatory; cytostatic; antimicrobial
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rat; pituitary; pituitrone; therapy; immune disorder; anaemia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12.7%; Score 33; DB 21; Length 262; 100.0%; Pred. No. 6.6e-20; Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  126 DDDPDAPAQLARALLRARLDPAALAAQLVPAP 158
    amino acid residue"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rat pituitary hormone, pituitrone.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAY71961 standard; Protein; 69 AA
                                                                                                                                                                                                                                                                 Claim 11; Fig 2; 277pp; English.
                                                                                                                                  (HUMA-) HUMAN GENOME SCI INC
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                                                                                27-APR-2000; 2000WO-US11211,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              26-MAR-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 100.
Matches 33; Conservative
                                                                                                                                                                                      WPI; 2000-687547/67.
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WP: 2000-687547/67.
DR N-PSDB: AAD02077.
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WP: 2000-687547/67.
DR N-PSDB: AAD02077.
XX
Nucleic acids encoding a novel pituitary hormone (pituitrone), useful for diagnosing, preventing and treating e.g. immune disorders, PT for diagnosing, preventing and treating e.g. immune disorders, PT for diagnosing, preventing and treating e.g. immune disorders.
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CC alm 11: Fig 2: 277pp; English.
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CC Staim 11: Fig 2: 277pp; English.
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CC Used as antigens in the production of antibodies against pituitrone or pituitrone is highly expressed in pituitary hormone, pituitrone.
CC used as antigens in the production of antibodies against pituitrone and in assays to identify modulators. Pituitrone converses in the production of antibodies against pituitrone and in assays to identify modulators. Pituitrone converses of the seases associated with inappropriate constitutive and renal system, immune disorders disorders of the manatopoletic cells (e.g., anaemia, bigecye syndrome, ataxia telanglectasia and Wiskott-Aidrich disorders, disorders of associated with inappropriate consistence in the solution of the solution
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Search completed: April 4, 2003, 14:28:29 Job time : 74 secs

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Gaps

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Perfect score:

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Database

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Human herpesvirus Streptomyces prist

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Oligonucleotide for Oligon

Human adenosine Al Oligonucleotide fo Oligonucleotide fo Oligonucleotide fo Oligonucleotide fo Mycobacterium tube Human low density Human low density Rabbit low density Rabbit low density Human hew density Human hew density Human hew density Aycobacterium tube HSV-2 immediate ea Human herpesvirus

oligonucleotide fo oligonucleotide fo oligonucleotide fo oligonucleotide fo Gene #1701 used to Kidney cancer rela cDNA encoding rat

CDNA encoding mous

Human secreted pro Human hydrophobic Human polynucleoti

Human; Tango-81; host cell; recombinant protein; antibody; receptor; specific binding agent; probe; primer; hybridisation; amplification; mutation; genetic mapping; ss. (MILL-) MILLENNIUM BIOTHERAPEUTICS INC Location/Qualifiers 58..840 /\*tag= a /product= "Tango-81" 97US-0054645. 98WO-US16241 WO9906427-A1. 04-AUG-1998; 04-AUG-1997; 11-FEB-1999

McCarthy SA;

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Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer; peripheral nervous system; neuropathy; central nervous system; CNS; Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic; amyotrophic lateral sclerosls; Shy-Drager Syndrome; chemotactic; chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
                                                                                                                                                                                                                                                                                           Novel nucleic acids and polypeptides, useful for treating disorders
                                                                                                                                                               GAGGCAGGCGACGACGCCGACGTGGACCCCCGAGCTGTTGAGGTACTTGCTGGGACGG
               ATTCTTGCGGGAAGCGCGGACTCCGAGGGGGTGGCAGCCCCCGCGCCGCCTCCGCCGTGCC
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Zhang
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Yang Y,
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Xu C, Xue AJ,
l, Drmanac RT;
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Goodrich R,
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25-APR-2000; 2000US-0553317.
9-JUL-2000; 2000US-0598042.
19-JUL-2000; 2000US-0653450.
14-SEP-2000; 2000US-0653450.
14-SEP-2000; 2000US-0653450.
29-NOV-2000; 2000US-063345.
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Wehrman T,
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P-PSDB; AAM39005.
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                                                                                                                               protein used in the method of the invention. Host cells containing the Tango protein are used to produce recombinant proteins for raising antibodies. It is also used in identifying specific binding agents (including cognate receptors), which can be used to determine amounts of recombinant protein in cells or therapeutically. Antibodies or other specific binding agents, are used to detect recombinant proteins and fragments of the Tango used to detect recombinant proteins and fragments for detecting the Tango gene, specifically mRNA, in usual hybridisation or amplification assays. These assays are used for diagnosis of diseases associated with abnormal expression of Tango proteins, e.g. detecting mutations in the Tango gene. Fragments of the Tango uncleic acid sequence are also used for genetic mapping and chromosome identification, and as antisense, riboxyme or triplex-forming therapeutics. Antibodies may also be used to generate
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                                                  New nucleic acid encoding human Tango-78, -79 and -81 proteins useful for diagnosis and treatment of Tango-associated diseases
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                                                                                                                                                                                                                                                                                                                                                                                              Score 977; DB 20; Length 979;
Pred. No. 8.9e-143;
0; Mismatches 0; Indels 0
                                                                                                                       This is the nucleotide sequence encoding the human Tango-81
                                                                                                                                                                                                                                                                                                                                                                       Sequence 979 BP; 112 A; 383 C; 346 G; 133 T; 5 other;
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                                                                                          Claim 1; Fig 3; 67pp; English.
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Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer peripheral nervous system; neuropathy; central nervous system; CNS; Alzheimer's; Parkinson's disease; Huntington's disease; heemostatic; amyotrophic lateral sclerosis; Shy Drager Syndrome; chemotactic; chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to human nucleic acids (AAI57798-AAI61369) and the encoded polypeptides (AAM38642-AAM42213) with nootropic,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        for treating disorders
  CGCGGACTCCGAGGGGTGGCAGCCCCGCGCGCCTCCGCCGTGCCGCCGACCACGATGT
                                                                                                   915 AGCACGTCCAGAGCAACTTACCCCGGCCAGCCAGCCTCTCACCCGAGGATCCCTACCCC
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Zhang J;
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Yang Y,
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Xue AJ,
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Wang Z, Wehrman T, Xu C, Xue AJ,
Zhou P, Goodrich R, Drmanac RT;
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                                                                                                                                                                                                                                                                                                                                                          AAI59947 standard; cDNA; 1041
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2000US-0552317.
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Wang J, V
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                                                  The invention relates to human nucleic acids (AAI57798-AAI61369) and the encoded polypeptides (AAM3642-AAM42213) with nootropic, immunosuppressant and cytostatic activity. The polynucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral nervous system, such as peripheral nervous system diseases, such as Alzheimer's Parkinson's disease. Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activities such as: Immune system suppression, and thrombolytic activity, chemotactic/chemokinetic activity, haemostatic assays for receptor activity, arthritis and inflammation, leukaemias and the construction of the activity, arthritis and inflammation, leukaemias and the construction of the activity, arthritis and inflammation, leukaemias and the construction of the activity, arthritis and inflammation, leukaemias and the construction of the activity, arthritis and inflammation, leukaemias and the construction of the construction of the activity, arthritis and inflammation.
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peripheral nervous system; neuropathy; central nervous system; CNS;
Alzheimer's; Parkinson's disease; Huntington's disease; heemostatic;
amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
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Wang Z, Wehrman T, Xu
Zhou P, Goodrich R,
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25-ARR-2000; 2000US-0552117.
09-JUL-2000; 2000US-0598042.
19-JUL-2000; 2000US-062312.
03-AUG-2000; 2000US-0653450.
14-SEP-2000; 2000US-0653450.
19-CT-20000; 2000US-0653450.
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ID AA159948 standard; cDNA; 1041
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Wang J, Wa
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                                                             Note: The sequence data for this patent did not form part of the printed specification.
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's disease;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present sequence is a cDNA clone HKGDL36 encoding human pituitary hormone, pituitrone. Pituitrone is highly expressed in pituitary gland and is also expressed in brain tissues, spinal cord and kidney. It may be used as antigens in the production of antibodies against pituitrone and in assays to identify modulators. Pituitrone cDNAs are also useful in gene therapy. Pituitrone may be used in the prevention, treatment and diseases associated with inappropriate pituitrone expression. It may be useful in treating disorders related to reproductive and renal system, immune disorders, disorders of the amenatopoletic cells (e.g., anamemia, Digeorge syndrome, ataxia telangiectasia and Wiskott-Aldrich disorder), blood coagulation disorders, autoimmune disorders (e.g. Addison's disease, multiple
164 CCGTGCACCCTGGGACCCAGAAGTGCCCCCGCCATCCCGCCACGAGGACTGCTCCCCGCC 105
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                               AGCACGTCCAGAGCAACTTACCCCGGCCAGCCAGCCTCTCACCCGAGGATCCCTACCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Human pituitary hormone, pituitrone"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nucleic acids encoding a novel pituitary hormone (pituitrone), for diagnosing, preventing and treating e.g. immune disorders, hyperproliferative disorders and blood coagulation disorders -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Mature human pituitary hormone,
                                                                                                                                                                                                                                                                                                                   cDNA encoding human pituitary hormone, pituitrone.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                  AAD02075 standard; cDNA; 1043 BP.
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                                         Sequence 1043 BP; 171 A; 391 C; 346 G; 135 T; 0 other;
                                                          Score 961.4; DB 21
Pred. No. 2.3e-140;
                                                      98.2%; Score .. 2.3e-, 99.4%; Pred. No. 2.3e-, ... 5; Mismatches
sclerosis and systemic lupus
disorders (e.g. neoplasms of
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AABB8606 (I) which have a hydrophobic domain. (I) have immunosuppressant, anti-live, neuroprotective, anti-lanaemic, vulnerary, anti-licer, anti-lifer, anti-inflammatory and cytostatic activities, and can be used in gene therapy. (I) can be used as pharmaceuticals and as antigens to prepare antibodies. DNA and cDNA (II) encoding (I) can be used aspected in gene therapy or for producing (I) in large quantities. Cells containing (II) are used for producing (I) in large quantities. Cells containing (II) are used for the detection of ligands or receptors corresponding to membrane or secretory proteins and to screen small molecule novel pharmaceuticals. Antibodies directed to (I) can be used for the detection, quantification and purification of (I). Activities of (I) may include cytokine and cell proliferation/differentiation function, immune stimulating or suppressing activity, haematopolesis regulating activity, tissue growth activity, activity, haematopolesis regulating activity, tissue growth activity, activity, receptor/ligand activity, and anti-inflammatory activity. (I) and (II) can be used to treat autoimmune disorders e.g. multiple sclerosis, HIV infections, anaemia, burns, ulcers, osteoporosis, continuamatory bowel disease and tumours. (I) and (II) can also be used for carbon or nitrogen source, to effect metabolism, catabolism, anabolism, processing and utilisation of dietary fat, protein, carbohydrate,
                                                                                                                                                                                                                                                                                           Human; hydrophobic domain; immunosuppressant; anti-HIV; neuroprotective; antianaemic; vulnerary; antiulcer; osteopathic; anti-inflammatory; cytostatic; gene therapy; autoimmune disorder; multiple sclerosis; HIV infection; anaemia; burn; ulcer; osteoporosis; tumour; wound healing; inflammatory bowel disease; nutritional supplement; appetite; vaccine; behavioural characteristic; immune response; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human proteins with hydrophobic domains and the DNAs which encode them are useful for treating autoimmune disorders, burns and tumors and for screening novel pharmaceuticals -
                                                                                                                                                                                                                                                        Human hydrophobic domain containing protein clone HP10756 cDNA #120.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 4; Page 461-463; 518pp; English.
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99JP-0252551.
99JP-0281132.
99JP-0301624.
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vitamins and minerals, to effect behavioural characteristics, to affect appetite, and can act as antigens in vaccines to raise an immune response to the protein or another material cross-reactive with the protein.
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                                                       198.0%; Score 959.8; 11arity 99.3%; Pred. No. 4e-1 Conservative 5; Mismatches
                                     Sequence 998 BP; 120 A; 394 C; 347
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The polynucleotide sequences given in AA298017 to AA298108 encode the human secreted proteins given in AAY87064 to AAX87223. Human secreted human secreted proteins given in AAY87064 to AAX87223. Human secreted compared to a protein can have activities based on the tissues and cells the genes are expressed in. Examples of activities include: cytostatic; cimhusouppressive; antiinflammatory; nootropic; neuroprotective; and activities include: cytostatic; cresponding secreted antialergic. The polynucleotides and their corresponding secreted polyneptides are useful for preventing, treating or ameliorating medical conditions, e.g. by protein or gene therapy. Also pathological conditions can be diagnosed by determining the amount of the new polypeptides in a conditions. As determining the presence of mutations in the new conditions. The man secreted protein s and their polynucleotides can be used for developing products for the diagnosis or treatment of cancer, tumours, neurodegenerative disorders, developmental abnormalities and forteimmune diseases, hepatic and renal disease, inflammation, altergies, Alzheimer's disease, behavioural disorders, schizophrenia, catchimmune diseases, hepatic and renal disease, inflammation, altergies, arthritis, infections, And Spinal cord injuries, transplant rejection, diabetes, asthma, sepsis, acne, psoriasis, cardiovascular disorders, and metabolic disorders. The

e.g.

New isolated human genes, useful for diagnosis and treatment of,

cancers, neurological or blood disorders Claim 1; Page 339; 494pp; English.

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antiinflammatory; nootropic; neuroprotective; antialiergic; cancer; tumour; neurodegenerative disorder; developmental abnormality; allergy; foetal deficiency; blood disorder; immune system disorder; arthritis; autoimmune disease; hepatic disease; renal disease; inflammation; Alzheimer's disease; behavioural disorder; schizophrenia; osteoporosis; infection; AIDS; spinal cord injury; transplant rejection; diabetes; asthma; sepsis; acne; psoriasis; cardiovascular disorder; respiratory disorder; metabolic disorder; food additive; preservative; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                   Shi Y;
Young PE;
                                                                                                                                                             Human; secreted protein; diagnosis; cytostatic; immunosuppressive;
                                                                                                                                        Human secreted protein encoding nucleotide sequence SEQ ID NO:58
                                                                                                                                                                                                                                                                                                                                                                                                                                   ), Rosen CA, Moore PA,
Brewer LA, Florence KA,
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Lafleur DW, Ebner R, Olsen HS, Brewer LA, F
Mucenski M, Endress GA, Soppet DR;
                                                                          BP
                                                                         AA298064 standard; cDNA; 1050
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                                                                                                                  (first entry)
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CTGGC 971
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15-JUL-1998;
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 CIGGC
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proteins or polynucleotides can also be used as food additives or
preservatives. The proteins are also useful for identifying their
binding partners. AAZ98008 to AAZ98016 and AAY87063 are sequence used
the exemplification of the present invention.
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                                                             Gaps
                                                                                GCCCAGCCAGTCCGCCSGYMCGRRGCCCGGCTCGCTGGGGGCAGCATGGCGGGGTCGCCGC 73
                                                                                                                                                               TGGCGCAGCTGCTGCGCGCTCTGGGCGCCCCCCGCAACTCTGATCCGGCTCTGGGCTTTGG
                                                                                                                                                                                                                                                                         CGTCTCCGCCCTTGGCTGAGACTGGCGCTCCTCGCCGCTTCCGGCGGTCAGTGCCCCGAG
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                                                                                                                                                                                                              AACGICAGGAGCGGGGGGGCGGAGGCGCAGGAGGCTGAGGATCAGCAGGCGCGCGTCC
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                                               DB 21; Length 1050;
                                                            Indels
                                 Sequence 1050 BP; 172 A; 398 C; 344 G; 136 T; 0 other;
                                              Score 912.8; DB 21;
Pred. No. 7.2e-133;
5; Mismatches 2;
                                                            5;
                                              93.2%;
                                                     Similarity 98.9
                                                            955;
                                               Query Match
                                                       Local
                                                            Matches
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AAD11630-AAD11721 represent cDNAs corresponding to 71 human secreted protein genes, and AAE06041-AAE06132 represent the proteins they encode. AAE06132-AAE06205 represent human secreted protein fragments.

The secreted proteins and their genes are useful for preventing, treating or ameliorating medical conditions, e.g., by protein or gene therapy. AEACHOGOGICAL conditions can be diagnosed by determining the amount of the new protein in a sample or by determining the presence of mutations in the new genes. Specific uses are described for each of the 71 genes, based on the tissues in which they are most highly expressed, and include developing products for the diagnosis or treatment of proliferative disorders, cancer, tumours, foetal and developmental abnormalities,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; secreted protein; proliferative disorder; cancer; tumour; asthma; foetal abnormality; developmental abnormality; haematopoietic disorder; immune system disorder; AIDS; autoimmune disease; rheumatobicatic disorder; Parkinson's disease; cognitive disorder; schizophrenia; skin disorder; psoriasis; sepsis; diabetes; atherosclerosis; cardiovascular disorder; inflammation; neurological disorder; Alzheimer's disease; food additive; angiogenic disorder; kidney disorder; psegnancy-related disorder; endocrine disorder; allergy; pregnancy-related disorder; endocrine disorder; infection; wound healing; cell culture; chemotaxis; vulnerary; binding partner identification;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human secreted protein-encoding gene 48 cDNA clone HKGDL36, SEQ ID NO:58
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Soppet DR;
907 CAGCACGICCAGAGCAACITACCCCGGCCAGCCAGCCTCTCACCCGAGGATCCCTACCC 966
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/product= "Human secreted protein precursor"
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Young PE,
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/product= "Mature human secreted protein"
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Florence KA,
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Brewer LA, F
M, Ebner R;
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55..501
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                                                                                                                                                                                                                                                                                                   BP.
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Endress GA, Muscenski M,
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154..498
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P-PSDB; AAE06088.
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                                                                                                       CCTGGC
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us-09-803-589-5.rng

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haematopoletic disorders, diseases of the immune system, AIDS, autoimmune diseases (e.g., rheumatoid arthritis), inflammation, allergies, neurobgical disorders (e.g., Alzheimmer's disease, Parkinson's disease), conditive disorders (e.g., Alzheimmer's disease, Parkinson's disease), conditive disorders, schizophrenia, asthma, skin disorders (e.g., and stone disorders, atherosclerosis, cardiovascular disorders, and sorders, independent disorders, endocrine disorders, and infections. The proteins can also be used to aid wound healing and epithelial cell proteins can also be used to aid wound healing and epithelial cell proliferation, to prevent skin aging due to sunburn, to maintain organs before transplantation, for supporting cell culture of primary tissues, to regenerate tissues, to identify their cognate ligands or binding partners, and in chemotaxis, and can be used as a food additive or preservative to modify storage properties. Antibodies specific for a content of the invention can be used in alleadismissible seguing with the disorders mentioned above, and in diagnostic immunoassays e.g., and other assay (ELISA).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              present sequence represents a human secreted protein-encoding cDNA of
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Sequence 1050 BP; 172 A; 398 C; 344 G; 136 T; 0 other;

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                                                                                                                                                                                                                    250 GTGAGGCGGGGGGGGGGGGGCG-GACCTGGCGGCGCGCGCGCGCATCTGCTGGA-GCCG 307
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                        Gaps
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                                                        11 GGCCAGCCAGCCGCCCGCCCGGCCCGGCTCGCTGGGGCAGCAGCAGCGGGGTCGCCGC 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14 GCCCAGCCAGTCCGCCSGYMCGRRGCCCGGCTCGCTGGGGGCAGCATGGCGGGGTCGCCGC
                                                                                                                                                                                    191 GTCTCCGCCCTTGGCT-AGACTGGCGCTCCTCGCCGCTTCCGGCGGCGGTCAGTGCCCCGAG
                                                                                                                                                                                                                                                               AACGTCAGGAGGGGCGGGGCGGAGGCGAGGAGGCTGAGGATCAGCAGGCGCGCGTCC
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Pred. No. 7.2e-133;
5; Mismatches 2; Indels 4;
 tch 93.2%; al Similarity 98.9%; 955; Conservative
            Local Similarity
  Query Match
                      Matches
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Human; ss; gene; secreted protein; gene therapy; immunosuppressive; antiarthritic; antirheumatic; antiproliferative; cytostatic; cardiant; vasotropic; cerebroprotective; nootropic; neuroprotective; antibacterial; virucide; fungicide; opthalmalogical; autoimmune disease; neoplasm; rheumatoid arthritis; hyperproliferative disorder; cardiac arrest; cardiovascular disorder; cerebral ischaemia; anglogenesis; nervous system disorder; Albeimer's disease; infection; ocular disorder; corneal infection; wound healing; skin aging; epithelial cell proliferation; food additive.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel 71 isolated secreted polypeptides and polynucleotides encoding the polypeptides, useful for treating Huntington's disease, sepsis, meningitis, thrombocytopaenia, haemolytic anaemia, rheumatoid arthritis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to an isolated nucleic acid molecule (or its fragment, homologue complement or allelic variant) encoding a human secreted protein (and its fragment, domain, epitope, variant, secreted form and species variant). Also included are a recombinant vector comprising the nucleic acid, a recombinant host cell comprising the
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Soppet 1
                                                          AGACCCGGGCGCCCCAGGTGCCTGCACCGCCTCTTGCCACCTGAGCACTGCCGGGT
                                                                                                                                                                                                    TGGGCTCTGAGCTGCCCCCTGAGGCGTGCTGGGGGCGCTGCTGCGTGTGAAACGCCTAG
                              TGGGCTCTGAGCTGCCCCCTGAGGGCGTGCTGGGGGGCGCTGCTGCTGAAACGCCTAG
                                                                                                                                                     847 CCCGTGCACCCTGGGACCCAGAAGIGCCCCCGCCATCCCGCCACCAGGACTGCTCCCCGC
                                                                                                                                                                                  914 CAGCACGTCCAGAGCAACTTACCCCGGCCAGCCAGCCTCTCACCCGAGGATCCCTACCC
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Young PE,
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Florence KA,
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Ebner R;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human secreted protein gene 48.
                                                                                                                                                                                                                                                                                                                                                      ABK69773 standard; cDNA; 1050
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                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
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Mucenski M,
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vector, an antibody against the secreted protein, a recombinant host cell that expresses the secreted protein and a method of identifying a binding partner of the secreted protein. The nucleic acid and protein are used to prevent, diagnose, treat or ameliorate a medical condition in e.g. prevent, ance, rabbits, goats, horses, cats, dogs, chickens or sheep for example autoimmune diseases e.g. rheumatoid arthritis, hyperproliferative disorders e.g. rheumatoid arthritis, cardiovascular disorders e.g. cardiac arrest, cerebroascular disorders e.g. cardiac arrest, cerebroascular disorders e.g. corneal infections caused by bacteria, viruses and fungi and calsorders e.g. corneal infections many other diseases and disorders e.g. corneal infection. The polypeptides can also be used to aid wound healing an epithelial cell proliferation, to prevent skin aging due to sunburn, to maintain organs before transplantation, for supporting cell culture of primary tissues, to regenerate tissues and in chemotaxis. The polypeptides can also be used as a food additive or preservative to increase storage capabilities. The present
                                                                                                                                                                                                                                                                                                                                                                                                                                                       373
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sequence encodes a novel human secreted protein of the invention
                                                                                                                                                                                                                                                                                                                   DB 24; Length 1050;
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                                                                                                                                                                                                                                                                                      Sequence 1050 BP; 172 A; 398 C; 344 G; 136 T; 0 other;
                                                                                                                                                                                                                                                                                                                   Score 912.8; DB 24
Pred. No. 7.2e-133;
5; Mismatches 2;
                                                                                                                                                                                                                                                                                                                   93.2%;
98.9%;
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AAF94417 to AAF94516 encode the human proteins given in AAB88557 to AAF88606 (I) which have a hydrophobic domain. (I) have immunosuppressant, anti-HIV, neuroprotective, antianaemic, vulnerary, antiulcer, osteopathic, anti-inflammatory and cytostatic activities, and can be used in gene therapy. (I) can be used as pharmaceuticals and as antigens to prepare antibodies. DNA and CDNA (II) encoding (I) can be used as probes for genetic diagnosis and gene sources for gene therapy or for
                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; hydrophobic domain; immunosuppressant; anti-HIV; neuroprotective; antianaemic; vulnerary; antiulcer; osteopathic; anti-inflammatory; cytostatic; gene therapy; autoimmune disorder; multiple sclerosis; HIV infection; anaemia; burn; ulcer; osteoporosis; tumour; wound healing inflammatory bowel disease; nutritional supplement; appetite; vaccine; behavioural characteristic; immune response; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human proteins with hydrophobic domains and the DNAs which encode them are useful for treating autoimmune disorders, burns and tumors and for screening novel pharmaceuticals -
                                                                                   846
                                                                                                             913
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                                                                                                                                                                                                                                                                                                                                                                                                           Human hydrophobic domain containing protein clone HP10756 cDNA #110.
                TGGGCTCTGAGCTGCCCCCTGAGGGCGTGCTGGGGGCGCTGCTGCGTGTGAAACGCCTAG
                                                       AGACCCCGGCGCCCCAGGTGCCTGCACGCCGCCTCTTGCCCACCCTGAGCACTGCCCGGAT
                                                                      CCCGTGCACCCTGGGACCCAGAAGTGCCCCCGCCATCCCGCCACCAGGACTGCTCCCCGC
                                                                                                                              CAGCACGTCCAGAGCAACTTACCCCGGCCAGCCAGCCTCTCACCCGAGGATCCCTACCC
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                                                                                                                                                                                                                                                                                                                           BP.
                                                                                                                                                                                                                                                                                                                         AAF94486 standard; cDNA; 780
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99JP-0252551.
99JP-0281132.
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P-PSDB; AAB88596.
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                                                                                                                                                                                                                          CCTGGC 979
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens.
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                                                                                                                                                                                                                                                   CCIGGC
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producing (I) in large quantities. Cells containing (II) are used for the detection of ligands or receptors corresponding to membrane or secretory proteins and to screen small molecule novel pharmaceuticals. Antibodies directed to (I) can be used for the detection, quantification and purification of (I). Activities of (I) may include cytokine and cell proliferation/differentiation function, immune stimulating or suppressing activity, haematopolesis regulating activity, tissue growth activity. CC activity, haematopolesis regulating activity, tissue growth activity. CC and thrombolytic activity, receptor/ligand activity and anti-inflammatory activity. (I) and (II) can be used to treat autoimmune disorders e.g. and thrombolytic activity in infections, anaemia, burns, ulcers, osteoporosis, inflammatory bowel disease and tumours. (I) and (II) can also be used for wound healing, as nutritional sources or supplements e.g. as amino acid, carbon or nitrogen source, to effect metabolism, catabolism, anabolism, processing and utilisation of dietary fat, protein, carbohydrate, contents and minerals, to effect behavioural characteristics, to affect the appetite and content and an another and another the protein or another material cross-reactive with the protein 88888888888888888888888888

Sequence 780 BP; 79 A; 297 C; 294 G; 110 T; 0 other;

ö 240 300 417 540 999 178 CGCGGCCTAAGCGCAGCGTCTCCGCCCTTGGCTGAGACTGGCGCTCCTCGCCGCTTCCGG 237 537 597 657 717 718 GCCGCCGACCACGATGTGGGCTCTGAGCTGCCCCCTGAGGGCGTGCTGGGGGCGCTGCTG 777 Gaps 658 CGGATTCTTGCGGGAAGCGCGGACTCCGAGGGGGGGGGCAGCCCCGCGCGCCTCCGCCGT GCCGCGCGCCTCCGACCCCGGCCCCCGGTCTACGACGACGGCCCCGGGGCCCGGGATGCT 598 GAGGAGGCAGGCGACGACACCCGACGTGGACCCCGAGCTGTTGAGGTACTTGCTGGGA CTCCGCGCCCGCCTTGACCCTGCCGCCCTAGCAGCCCAGCTTGTCCCCGCGCCCGTCCCC ó Length 780; Indels 79.3%; Score 776.8; DB 22; 99.7%; Pred. No. 7.5e-112; 0; Mismatches 778; Conservative Local Similarity Query Match Matches 28 478 538 238 298 418 g a g g q g g g ò g ò ŏ ò ò ò ò à g δ ò g ò

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assays for receptor activity, arthritis and inflammation, C.N.S disorders.
Note: The sequence data for this patent did not form part

Sequence 919 BP; 122 A; 365 C; 308 G; 124 T; 0 other;

specification.

DB 22; Length 919;

5%; Score 729.4;

Query Match

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The Invention relates to human nucleic acids (AAI57798-AAI61369) and the encoded polypeptides (AAM36642-AAM42213) with nootropic, immunosuppressant and cytostatic activity. The polynucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral nervous asystem, such as peripheral nervous system, such as modentral nervous system, such as peripheral nervous system diseases, unot as Alzhehmer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activities such as: Immune system suppression, Activin/inhibin activity, chemoteactic/chemokinetic activity, haemostatic and thrombolytic activity, arthritis and inflammation, leukaemias and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ä
                                                                                                                                                                                                                                           peripheral nervous system; neuropathy; central nervous system; CNS; Alzheimer's; Parkinson's disease; hautington's disease; haemostatic; amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic; chemotic; thrombolytic; drug screening; arthritis; inflammation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Wang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel nucleic acids and polypeptides, useful for treating disorders such as central nervous system injuries .
               778 CGTGTGAAACGCCTAGAGACCCCGGCGCCCCAGGTGCCTGCACGCCGCCTCTTGCCACCC
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Yang Y,
                                                                                                                                                                                                                               cytostatic;
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Wang Z, Wehrman T, Xu C, Xue AJ,
Zhou P, Goodrich R, Drmanac RT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; SEQ ID NO 365; 10078pp; English.
                                                                                                                                                                                                                               nootropic; immunosuppressant;
                                                                                                                                                                                                Human polynucleotide SEQ ID NO 365.
                                                                                                       BP
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20000S-0653450.
2000US-0662191.
2000US-0663036.
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2000US-0552317.
2000US-0598042.
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P-PSDB; AAM39006.
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                                                                                                                                                                                                                                                                                                        leukaemia; ss.
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09-JUL-2000;
19-JUL-2000;
03-AUG-2000;
14-SEP-2000;
19-OCT-2000;
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AAD02076 standard; cDNA; 991

AAD02076

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   795 GACCCCGGCGCCCCAGGTGCCTGCACGCCGCCTCTTGCCACCCTGAGCACTGCCCGGATC 854
         Gaps
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                                 GCCAGCCAGTCCGCCSGYMCGRRGCCCGGCTCGCTGGGGCAGCATGGCGGGGTCGCCGCT
                                                                                          TCGGCCGCCCCCCCCGCGCTCTGCGCGGCCGGGTAAAGGAGCCCCGCGGGCCTAAGCGCAGC
                                                                                                  210 GTCTCCGCCCTTGGCTGAGACTGGCGCTCCTCGCCGCTTCCGGCGGCGGTCAGTGCCCCGAGG
                                                                                                                                                                                                      GTCTCCGCCCTTGGCTGAGACTGGCGCTCCTCGCCGCTTCCGGCGGTCAGTGCCCCGAGG
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        Indels 111;
ed. No. 1.5e-104;
Mismatches 1;
Pred.
87.98;
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Similarity
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The present sequence is a cDNA encoding mouse pituitary hormone, pituitrone. Pituitrone is highly expressed in pituitary gland and is also expressed in brain tissues, spinal cord and kidney.

It may be used as antigens in the production of antibodies against pituitrone and in assays to identify modulators. Pituitrone cDNAs are also useful in gene therapy. Pituitrone may be used in the prevention, treatment and diagnosis of diseases associated with inappropriate pituitrone expression. It may be useful in treating disorders related to reproductive and renal system, immune disorders, disorders of haematopoietic cells (e.g., anaema, blageorge syndrome, ataxia telangiectasia and Wiskott-Aldrich disorder), blood coagulation disorders, autoimmune disorders (e.g., Addison's disease, multiple sclerosis and systemic lupus erythematosus (E.E.), hyperproliferative disorders (e.g. neoplasms of bone, liver and pancreas) and infectious
                                                                                                        Mouse; pituitary; pituitrone; therapy; immune disorder; anaemia; Digeorge syndrome; haematopoietic cell; ataxia telangiectasia; Wiskott-Aldrich disorder; blood coagulation disorder; Addison's disease; autoimmune disorder; multiple sclerosis; systemic lupus erythematosus; SLE; hyperproliferative disorder; gene therapy; neoplasm; infectious disease; immunomodulatory; cytostatic; antimicrobial; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    pituitrone"
                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Mature mouse pituitary hormone, pituitrone
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                                                                                                                                                                                                                                                                                                      "Mouse pituitary hormone, pituitrone"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nucleic acids encoding a novel pituitary hormone (pituitrone), for diagnosing, preventing and treating e.g. immune disorders, hyperproliferative disorders and blood coagulation disorders -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /product= "Mature mouse pituitary hormone, /note= "An alternative mature protein referred in page 11"
                                                                                                                                                                                                                                                                                                                                    /*tag= b
/note= "An alternative leader sequence
                                                                              pituitrone
                                                                              cDNA encoding mouse pituitary hormone,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; Page 266-268; 277pp; English.
                                                                                                                                                                                                                                                                                                                                                                      referred in page 11"
                                                                                                                                                                                                                                                        Location/Qualifiers
59..835
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                                              (first entry)
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158..832
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                                                                                                                                                             GTCTCCGCCCTTGGCTGAGACTGGCGCTCCTCGCCGCTTCCGGCGGTCAGTGCCCCGAGG
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                                         7;
                         Length 991;
                        Score 565.4; DB 21; Length
Pred. No. 3.3e-79;
5; Mismatches 184; Indels
        G; 153 T; 0 other;
        315
        ပ်
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                        Query Match 57.8%;
Best Local Similarity 78.1%;
Matches 698; Conservative
        A; 365
        BP; 158
        Sequence 991
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fragment, homologue complement or allelic variant, encoding a human secreted protein (and its fragment, domain, epitope, variant, secreted form and species variant). Also included are a recombinant vector comprising the nucleic acid, a recombinant host cell comprising the nucleic acid, a recombinant host cell comprising the centor, an antibody against the secreted protein, a recombinant host cell that expresses the secreted protein and a method of identifying a binding partner of the secreted protein. The nucleic acid and protein are used to partner of the secreted protein. The nucleic acid and protein are used to prevent, diagnose, treat or ameliorate a medical condition in e.g. humans, mice, rabbits, goats, horses, cats, dogs, chickens or sheep for example autoimmune diseases e.g. rheumatoid arthritis, cardiovascular disorders e.g. cardiac arrest, cerebrovascular disorders e.g. cardiac arrest, cerebrovascular disorders e.g. cardiac arrest, cerebrovascular disorders e.g. corneal infections caused by bacteria, viruses and fungi and coular disorders e.g. corneal infection. Many other diseases and classification the polypeptides can also be used to aid wound healing an epithelial cell proliferation, to prevent
                                                                                        Human; ds; secreted protein; gene therapy; immunosuppressive; antiarthritic; antirheumatic; antiproliferative; cytostatic; cardiant; assotropic; cerebroprotective; nontoprotective; antibacterial; virucide; fungicide; opthalmalogical; autoimmune disease; neoplasm; rheumatoid arthritis; hyperproliferative disorder; cardiac arrest; cardiovascular disorder; cerebroal ischaemia; angiogenesis; nervous system disorder; Alzheimer's disease; infection; coular disorder; corneal infection; wound healing; skin aging; epithelial cell proliferation; food additive.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  skin aging due to sunburn, to maintain organs before transplantation, for supporting cell culture of primary tissues, to regenerate tissues and in chemotaxis. The polypeptides can also be used as a food additive or preservative to increase or decrease storage capabilities. The present sequence represents a ds DNA fragment of the gene for a novel human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               the polypeptides, useful for treating Huntington's disease, sepsis, meningitis, thrombocytopaenia, haemolytic anaemia, rheumatoid arthritis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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Soppet D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to an isolated nucleic acid molecule (or its
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Young PE,
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                                                        Human secreted protein gene 49 genomic DNA fragment #2.
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Pred. No. 3.3e-65;
0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  , Rosen CA,
Florence KA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel 71 isolated secreted polypeptides and
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Komatsoulis G, Duan v. Pr
Prewer LA, F'
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                     entry)
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Best Local Similarity 99.4<sup>†</sup>
Matches 476; Conservative
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Endress GA,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human, cytosine methylation; 5'-CpG-3'; uracil; cytosine; diagnosis;
drug. side effect; cancer; central nervous system; cardiovascular;
gastrointestinal; respiratory system; single nucleotide polymorphism;
                                                                                                                                                                                                                                                                                           648
                                                                                                                                                                                                                                                                                                                                                                                                                                      Oligonucleotide for detecting cytosine methylation SEQ ID NO 17745.
                                  AGGAGCCCCGCGCGCCTAAGCGCAGCGTCTCCCGCCCTTGGCTGAGACTGGCGCTCCTCGCC
                                                                   CGCTGGCGCATCTGCTGGAGGCCGAACGTCAGGAGCGGGCGCGGGGCCGAGGCGCAGGAGG
                                                                               CTGAGGATCAGCAGGCGCGCGTCCTGGCGCAGCTGCTGCGCGCTTTGGGGCGCCCCCCGCA
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05-SEP-2000; 2000DE-1044543.
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cytosine (C) but not methylated C, to uracil, then part of the genomic DNA that contains the target C is amplified to form a labeled amplicon. The amplicon is hybridised to two classes, each with at least one member, of oligonuclectides and/or peptide-nucleic acid (PNA) oligomers and the degree of hybridisation to both classes is determined from the label on the amplicon. From the ratio of labels hybridised to the two classes of oligomers, the degree of methylation is calculated. The method is used: (1) for diagnosis and/or prognosis of side effects of the rapeutic drugs and of a wide range of diseases, e.g. cancer, disorders of the central nervous, cardiovascular, gastrointestinal and respiratory systems etc., particularly by detecting mutations or single nucleotide polymorphisms (SNP's); and (11) for differentiation of cell or tissue types and for investigating cell differentiation. The method allows the methylation status of many c residues to be determined simultaneously. ABG1310-ABG54121 represent genomic DNA sequences used to illustrate the method for determining the degree of cytosine methylation described in
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                                                                                                                      The method
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                                                                                                                                                                                                                                                                                                                                                                                 Length 652;
                                                                                                                                                                                                                                                                                                                                                                               Query Match 30.8%; Score 301.6; DB 24; Length Best Local Similarity 77.1%; Pred. No. 1.9e-38; Matches 367; Conservative 0; Mismatches 109; Indels
                                                                                                                                                                                                                                                                                                                                             Sequence 652 BP; 103 A; 81 C; 233 G; 235 T; 0 other;
                                                                                                                                                                                                                                                                                                            the disclosure of the invention.
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Human, cytosine methylation; 5'-CpG-3'; uracil; cytosine; diagnosis; drug; side effect; cancer; central nervous system; cardiovascular; gastrointestinal; respiratory system; single nucleotide polymorphism; SNP; cell differentiation; ds. Oligonucleotide for detecting cytosine methylation SEQ ID NO 17746. 

BP

ABQ31155 standard; DNA; 652

ABQ31155

(first entry)

12-JUL-2002 ABQ31155;

Homo sapiens

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of in

This invention describes a novel method for determining the degree methylation of a particular cytosine in a motif 5'-CpG-3', present genomic sample of DNA. The sample is treated chemically to convert

Claim 12; 56pp + Sequence Listing; 56pp; German.

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Guetig D;
                                                                                                                                                                                  Berlin K,
                                                               01-SEP-2001; 2001WO-EP10074.
                                                                                               01-SEP-2000; 2000DE-1043826.
                                                                                                                                                                                  Olek A, Piepenbrock C,
                                                                                                                                                 (EPIG-) EPIGENOMICS AG
                                                                                                                                                                                                                WPI; 2002-371829/40.
WO200218632-A2.
                                07-MAR-2002
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methylation of a particular cytosine in a motif 5'-cp6-3', present in a genomic sample of DNA. The sample is tracted chemically to convert cytosine (C) but not methylated C, to uracil, then part of the genomic DNA that contains the target C is amplified to form a labeled amplicon. The amplicon is hybridised to two classes, each with at least one member, of oligonocleotides and/or peptide nucleic acid (NNA) oligomers and the degree of hybridisation to both classes is determined from the Label on the amplicon. From the ratio of labels hybridised to the two classes of oligomers, the degree of methylation is calculated. The method is used: (1) for diagnosis and/or prognosis of side effects of therapeutic drugs and of a wide range of diseases, e.g. cancer, disorders of the central nervous, cardiovascular, gastrointestinal and respiratory systems etc., particularly by detecting mutations or single nucleotide polymorphisms (SNP's); and (ii) for differentiation. The method allows the methylation status of many C residues to be determined simultaneously.

ABQ13410-ABQ54121 represent genomic DNA sequences used to illustrate the method for determining the degree of cytosine methylation described in the degree of cytosine methylation described in Determining the degree of cytosine methylation in genomic DNA, useful for diagnosis and prognosis, comprises selective hybridization of amplicons from chemically treated DNA This invention describes a novel method for determining the degree Claim 12; 56pp + Sequence Listing; 56pp; German. the disclosure of the invention. 

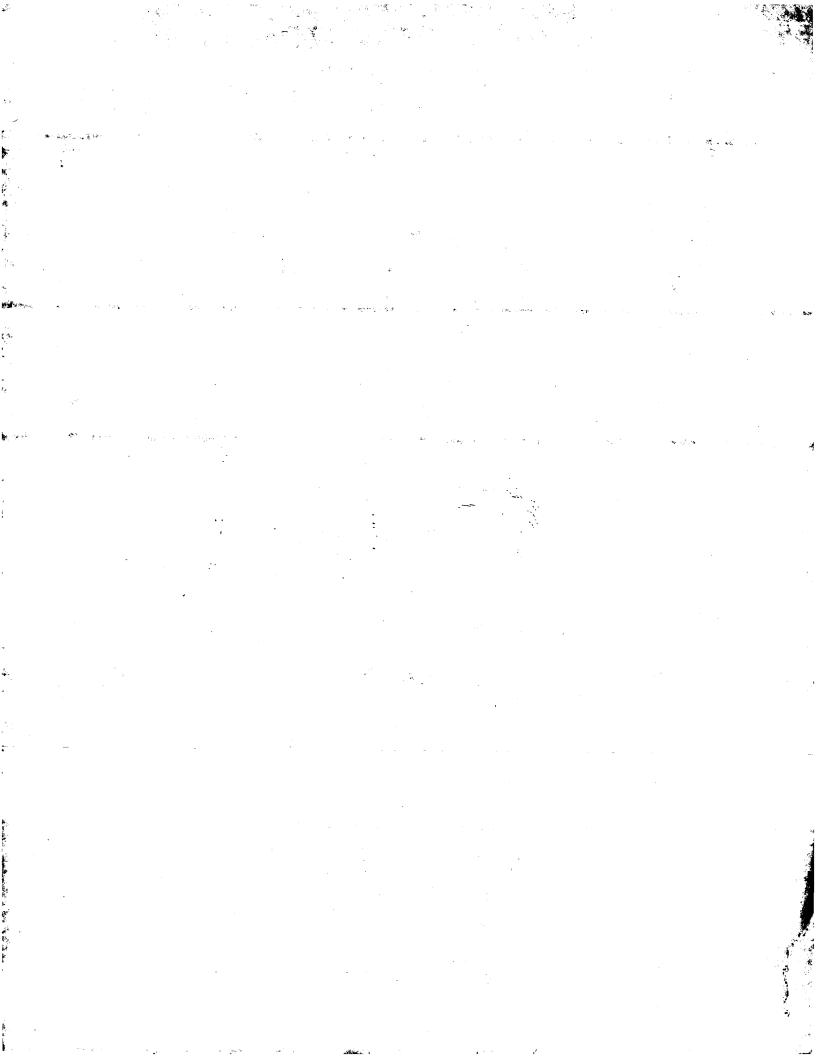
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Sequence 652 BP; 235 A; 233 C; 81 G; 103 T; 0 other;

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   DB 24; Length 652;
Score 301.6; DB 24; Length
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Best Local Similarity 77.1%;
Matches 367; Conservative (
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Aujeszky's disease Drosophila melanog

New nucleic acid encoding human Tango-78, -79 and -81 proteins useful for diagnosis and treatment of Tango-associated diseases

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Human Human

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Human neuregulin

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Human; Tango-81; host cell; recombinant protein; antibody;
receptor; specific binding agent; probe; primer; hybridisation;
amplification; mutation; genetic mapping.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Amino acid sequence of the human Tango-81 protein.
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WPI; 1999-153693/13.
N-PSDB; AAV68668.
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            GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
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                             This is the amino acid sequence of the human Tango-81 protein used in the method of the invention. Host cells containing the Tango protein are used to produce recombinant proteins for raising antibodies. It is also used in identifying specific binding agents (including cognate receptors), which can be used to determine amounts of recombinant protein in cells or therapeutically. Antibodies or other specific binding agents, are used to detect recombinant proteins and fragments of the Tango concerns be used as probes or primers for detecting the Tango gene, specifically mRNA, in usual hybridisation or amplification assays. These assays are used for diagnosis of diseases associated with abnormal expression of Tango proteins, e.g., detecting mutations in the Tango gene. Fragments of the Tango
                                                                                                                                                                            nucleic acid sequence are also used for genetic mapping and chromosome identification, and as antisense, ribozyme or triplex forming therapeutics. Antibodies may also be used to generate
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                                                                                                                                                                                                                                                             Length 260;
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100.0%; Pred. No. 2.9e-104;
ive 0; Mismatches 0; 1
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/label- Signal_peptide
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/label- Mature_human_pituitrone
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           Claim 1; Fig 3; 67pp; English.
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                                                                                                                                                                                                                anti-idiotype antibodies.
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Best Local Similarity 100.
Matches 260; Conservative
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The present sequence is a human pituitary hormone, pituitrone (clone HKGDL36). Pituitrone is highly expressed in pituitary gland and is also expressed in brain tissues, spinal cord and kidney. It may be used as antigens in the production of antibodies against pituitrone and in assays to identify modulators. Pituitrone cDNAs are also useful in gene therapy. Pituitrone may be used in the prevention, treatment and diagnosis of diseases associated with inappropriate pituitrone expression. It may be useful in treating disorders related to reproductive and renal system, immune disorders, disorders of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nucleic acids encoding a novel pituitary hormone (pituitrone), useful for diagnosing, preventing and treating e.g. immune disorders, hyperproliferative disorders and blood coagulation disorders -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           disorders, autoimmune disorders (e.g. Addison's disease, multiple
sclerosis and systemic lupus erythematosus (SLE)), hyperproliferative
disorders (e.g. neoplasms of bone, liver and pancreas) and infectious
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121 PALGLDDDPDAPAAQLARALLRARLDPAALAAQLVPAPVPAAALRPRPPVYDDGPAGPDA 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           haematopoietic cells (e.g., anaemia, Digeorge syndrome, ataxia telangiectasia and Wiskott-Aldrich disorder), blood coagulation
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Pred. No. 2.9e-104;
Mismatches 0;
                                                                                                                                                                                                                                         /note= "Highly - 206..211 '--te= "Highly immunogenic"
                                                                                             "Highly immunogenic"
                                                                                                                                                   "Highly immunogenic"
                                                                                                                                                                                                      "Highly immunogenic"
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"Highly immunogenic"
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100.0%;
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253..258
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                                                                        116..121
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185..19
                                                                                                                                                   /note=
164..18
'note"
                                                                                                     /note=
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PROTEGENE INC
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N-PSDB; AAF94486.
                                             Similarity
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              260 AA;
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                                   Query Match
Best Local Simi
Matches 260;
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01-OCT-1999;
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              Sequence
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ID AAB8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to human nucleic acids (AAIS7798-AAI61369) and the encoded polypeptides (AAM36642-AAM42213) with nootropic, immunosuppressant and cytostatic activity. The polynucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral nervous system autopathies and central nervous system diseases, such as lazhelmer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activities such as: Immune system suppression, Activinianian activity, chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, cancer diagnosis and therapy, drug screening, as assays for receptor activity, arthritis and inflammation, leukaemias and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Note: The sequence data for this patent did not form part of the printed specification.
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peripheral nervous system; neuropathy; central nervous system; CNS; Alzheimer's; Parkinson's disease; haurtington's disease; haemostatic; amyotrophic lateral sclercists; Shy-brager Syndrome; chemotactic; chemotactic; thrombolytic; drug screening; arthritis; inflammation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Wang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel nucleic acids and polypeptides, useful for treating disorders such as central nervous system injuries -
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Zhang J;
                                                                                                                                                                                                                Human; nootropic; immunosuppressant; cytostatic; gene therapy;
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Yang Y,
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Wehrman T, Xu C, Xue AJ,
Goodrich R, Drmanac RT;
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                                                                                                                        AAM39005 standard; Protein; 260 AA.
                                                                                                                                                                                           Human polypeptide SEQ ID NO 2150.
                                                        RVKRLETPAPQVPARRLLPP 260
                                                                                                                                                                                                                                                                                                                                                                                   2000US-0488725.
2000US-0552317.
2000US-0598042.
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2000US-0653450.
2000US-0662191.
2000US-0693036.
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29-NOV-2000; 2000US-0727344
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                                                                                                                                                                     (first entry)
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N-PSDB; AAI58161.
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Wang Z, W
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                                                                                                                                                                                                                                                                                                                  WO200153312-A1.
                                                                                                                                                                                                                                                                                             Homo sapiens.
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03-AUG-2000;
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09-JUL-2000;
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                                                                                                                                                                                                                                                              RSVPRGEAAGAVQELARALAHLLEAERQERARAEAQEAEDQQARVLAQLLRVWGAPRNSD 120
                                                                                                                                                                                                                                                                                                                                              PALGLDDDPDAPAAQLARALLRARLDPAALAAQLVPAPVPAAALRPRPPVYDDGPAGPDA 180
                                                                                                                                                                                                                                                                                                                                                                                                       PALGLDDDPDAPAAQLARALLRARLDPAALAAQLVPAPVPAAALRPRPFVYDDGPAGPDA 180
                                                              Gaps
                                                                                                              1 MAGSPLLWGPRAGGVGLLVLLLLGLFRPPPALCARPVKEPRGLSAASPPLAETGAPRFFR 60
                                                                                                                                               EEAGDETPDVDPELLRYLLGRILAGSADSEGVAAPRRLRRAADHDVGSELPPEGVLGALL
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  Length 260;
                                                           Indels
100.0%; Score 1319; DB 22;
100.0%; Pred. No. 2.9e-104;
ive 0; Mismatches 0; 1
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99JP-0281132
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                                                           Conservative
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CC AAE9417 to TaAE94516 encode the human proteins given in AAB88557 to AAE98606 (I) which have a hydrophobic domain. (I) have immunosuppressant, costeopathic, anti-inflammatory and cytostatic activities, and can be used as paramaceuticals and as antigens used in gene therapy. (I) can be used as paramaceuticals and as antigens to prepare antibodies. DNA and cDNA (II) encoding (I) can be used as probes for genetic diagnosis and gene sources for gene therapy or for probes for genetic diagnosis and gene sources for gene therapy or for corpucting (I) in large quantities. Cells containing (II) are used for the detection of ligands or receptors corresponding to membrane or secretory proteins and to screen small molecule novel pharmaceuticals.

CX Antibodies directed to (I) can be used for the detection, quantification and purification of (I). Activities of (I) may include cytokine and cell proliferation/differentiation function, immune stimulating or suppressing activity, haematopolesis regulating activity, tissue growth activity.

CX antibodies directions are receptor/ligand activity and anti-inflammatory cativity. (I) and (II) can be used to treat autoimmune disorders e.g. multiple sclerosis, HIV infections, anaemia, burns, ulcers, osteoporosis, conflammatory bowel disease and tumours. (I) and (II) can also be used for wound healing, as nutritional sources or supplements e.g. as amino acid, carbon or nitrogen source, to effect metabolism, catabolism, and dullisation of dietary fat, protein, carbohydrate, cuthamins and minerals, to effect behavioural characteristics, to affect appetite, and can act as antigens in vaccines to raise an immune response con the protein or another material cross-reactive with the protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RSVPRGEAAGAVQELARALAHLLEAERQERARAEAQEAEDQQARVLAQLLRVWGAPRNSD 120
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0
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the encoded polypeptides (AAM38642-AAM42213) with nootropic, immunosuppressant and cytostatic activity. The polynuclectides are useful in gene therapy. A composition containing a polypeptide or polynuclectide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activities such as Immune system suppression, Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, cancer diagnosis and therapy, drug screening, assays for receptor activity, arthritis and inflammation, leukaemias and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The sequence data for this patent did not form part of the printed
                                                                                                                                                                                                                                            Wang D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RSVPRGEAAGAVQELARALAHLLEAERQERARAEAQEAEDQQARVLAQLLRVWGAPRNSD 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EEAGDETPDVDPELLRYLLGRILAGSADSEGVAAPRRLRRAADHDVGSELPPEGVLGALL 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9
                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to human nucleic acids (AAI57798-AAI61369) and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MAGSPLINGPRAGGYGLLVLLLLGLFRPPPALCARPVKEPRGLSAASPPLAETGAPRFFR 60
                                                                                                                                                                                                                                                                                                                                              Novel nucleic acids and polypeptides, useful for treating disorders such as central nervous system injuries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PALGLDDDPDAPAAQLARALLRARLDPAALAAQLVPAPVPAAALRPRPPVYDDGPAGPDA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         83.8%; Score 1105.5; DB 22; Length 223;
85.8%; Pred. No. 3.4e-86;
1ive 0; Mismatches 0; Indels 37;
                                                                                                                                                                                                                                            Qian XB,
Yang Y,
                                                                                                                                                                                                                                          Chen R, Ma Y,
Xu C, Xue AJ,
                                                                                                                                                                                                                                                                                                                                                                                          Example 4; SEQ ID NO 2151; 10078pp; English.
                                                                                                                                                                                                                                                          Xu C, Xue AJ
Drmanac RT;
                                                                                                                                                                                                                                        Liu C, Asundi V, Che
Wang Z, Wehrman T, Xt
Zhou P, Goodrich R,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EEAGDETPDVDPELLRYL-----
                                                                                                                     2000US-0620312.
2000US-0653450.
2000US-0662191.
2000US-0693036.
                                           26-DEC-2000; 2000WO-US34263
                                                                                                       2000US-0598042
                                                                                                                                                                                2000US-0727344
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Best Local Similarity 85.8
Matches 223; Conservative
                                                                                                                                                                                                                                                                                                  WPI; 2001-442253/47.
N-PSDB; AAI58162.
                                                                                                                                                                                                              (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               223 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C.N.S disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 specification.
                                                                                                                                                                               29-NOV-2000;
                                                                                                                                                  14-SEP-2000;
19-OCT-2000;
                                                                                                                   19-JUL-2000;
                                                                                                       09-JUL-2000;
                                                                                          25-APR-2000;
               26-JUL-2001
                                                                                                                                                                                                                                        Tang YT;
Wang J, F
Zhao QA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
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RESULT 6

WO200153312-A1

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Gaps

AAY71960;

AAY71960

Peptide

ds sn é Peptide Protein Protein

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Rat; human; mouse; pituitary; pituitrone; therapy; immune disorder; Digeorge syndrome; haematopoletic cell; ataxia telangiectasia; Wiskott-Aldrich disorder; blood coagulation disorder; Addison's disease; autoimmune disorder; multiple sclerosis; systemic lupus erythematosus; SLE; hyperproliferative disorder; gene therapy; neoplasm; anaemia;
                                                                                                                      PALGLDDDPDAPAAQLARALLRARLDPAALAAQLVPAPVPAAALRPRPPVYDDGPAGPDA 180
                                                                                                                                                                                               EEAGDETPDVDPELLRYLLGRILAGSADSEGVAAPRRLRRAADHDVGSELPPEGVLGALL 240
                                                                                                      RSVPRGEAAGAVQELARALAHLLEAERQERARAEAQEAEDQQARVLAQLLRVWGAPRNSD 120
                                 MAGSPLLWGPRAGGVGLLVLLLLGLFRPPALCARPVKEPRGLSAASPPLAETGAPRFR 60
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39; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Consensus sequence of human, mouse and rat pituitrone.
 Mismatches
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13;
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                                                                                                                                                                                                                                                                                                                                      (first entry)
Conservative
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Misc-difference 57
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Matches 206;
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                                                                                                                                                    Mouse; pituitary; pituitrone; therapy; immune disorder; anaemia; Digeorge syndrome; haematopoietic cell; ataxia telangiectasia; Wiskott-Aldrich disorder; blood coagulation disorder; Addison's disease; autoimmune disorder; multiple sclerosis; systemic lupus erythematosus; SLE; hyperproliferative disorder; gene therapy; neoplasm; infectious disease; immunomodulatory; cytostatic; antimicrobial.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present sequence is a mouse pituitary hormone, pituitrone. Pituitrone is highly expressed in pituitary gland and is also expressed in brain tissues, spinal cord and kidney. It may be used as antigens in the production of antibodies against pituitrone and in assays to identify modulators. Pituitrone cDNAs are also useful in gene therapy. Pituitrone may be used in the prevention, treatment and diagnosis of diseases associated with inappropriate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           pituitrone expression. It may be useful in treating disorders related to reproductive and renal system, immune disorders, disorders of haematopoietic cells (e.g., anaemia, Digeorge syndrome, ataxia telangiectasia and Wiskott-Aldrich disorder), blood coagulation disorders, autoimmune disorders (e.g. Addison's disease, multiple sclerosis and systemic lupus erythematosus (SLE)), hyperproliferative disorders (e.g. neoplasms of bone, liver and pancreas) and infectious
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            useful
                                                                                                                                                                                                                                                                                                                                                                                                                                        /note= "Mature mouse pituitrone"
/note= "An alternative mature protein referred in
page 11"
                                                                                                                                                                                                                                                                                                                                                                      signal sequence referred
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nucleic acids encoding a novel pituitary hormone (pituitrone), for diagnosing, preventing and treating e.g. immune disorders, hyperproliferative disorders and blood coagulation disorders -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 1019; DB 21; Length 258;
Pred. No. 9.2e-79;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 34..258
/note= "Mature mouse pituitrone"
                                                                                                                                                                                                                                                                                                                                                                    /note= "An alternative
                                                                                                                                                                                                                                                                                                                                            ...34
/label= Signal_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                ...33
/label= Signal_peptide
                                                                                                                   Mouse pituitary hormone, pituitrone.
                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
            AAY71960 standard; Protein; 258 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 11; Fig 2; 277pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (HUMA-) HUMAN GENOME SCI INC
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79.28;
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                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                     11
                                                                                                                                                                                                                                                                                                                                                                                          page
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                                                                                 26-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          09-NOV-2000
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Ruben SM,

Sequence

Query Match

diseases

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Human; secreted protein; proliferative disorder; cancer; tumour; asthma; foctal abnormality; developmental abnormality; hematopoietic disorder; immune system disorder; AIDS; autoimmune disease; rheumatoid arthritis; Parkinson's disease; cognitive disorder; schlzophrenia; skin disorder; parkinson's disease; cognitive disorder; schlzophrenia; skin disorder; inflammation: neurological disorder; Alzheimer's disease; food additive; anglogenic disorder; kidney disorder; gastrointestinal disorder; allergy; prepanary related disorder; endocrine disorder; infection; wound healing; gene therapy.
                                                     The present sequence is a consensus sequence of human, mouse and rat pituitrone. Pituitrone is highly expressed in pituitary gland and is also expressed in brain tissues, spinal cord and kidney. Pituitrone may be used as antigons in the production of antibodies against pituitrone and in assays to identify modulators. Pituitrone cDNAs are also useful in gene therapy. Pituitrone may be used in the prevention, treatment and diagnosis of diseases associated with inappropriate
                                                                                                                                                       pitultrone expression. It may be useful in treating disorders related to reproductive and renal system, immune disorders, disorders of haematopoletic cells (e.g., anaemia, Digeorge syndrome, ataxia telangiectasia and Wiskott-Aldrich disorder), blood coagulation disorders, autoimmune disorders (e.g. Addison's disease, multiple sclerosis and systemic lupus erythematosus (SLE), hyperproliferative disorders (e.g. neoplasms of bone, liver and pancreas) and infectious
                                                                                                                                                                                                                                                                                                                                                                                                                          RSVPRGEAAGAVQELARALAHLLEAERQERARAEAQEAEDQQARVLAQLIRVWGAPRNSD 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MAGSPLLWGPRAGGVGLLVLLLLGLFRPPPALCARPVKEPRGLSAASPPLAETGAPRFFR 60
                                                                                                                                                                                                                                                                                                                                                                                  RXVPRGEAAGAVQELARAXAXXLEAERQERARAEAQEAEDQQARVLAXLLXXWGXPRXSD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PALGLDDDPDAPAAQLARALLRARLDPAALAAQLVPAAALRPRPPVYDDGPAGPDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EEAGDETPDVDPELLRYLLGRILAGSADSEGVAAP - - RRLRRAADHDVGSELPPEGVLGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human gene 48 encoded secreted protein HKGDL36, SEQ ID NO:150.
                                                                                                                                                                                                                                                                                                            Length 262;
  hyperproliferative disorders and blood coagulation disorders
                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                           77.0%; Score 1015; DB 21;
llarity 80.2%; Pred. No. 2e-78;
Conservative 3; Mismatches 47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1..33
/label= Signal_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAE06088 standard; Protein; 148 AA.
                              Fig 2; 277pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LLRVKRLETPAPQVPARRLLPP 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                       Best Local Similarity
Matches 210; Conserv
                                                                                                                                                                                                                                                                                  262 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
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                                                                                                                                                                                                                                                          diseases.
                                                                                                                                                                                                                                                                                    Sequence
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                                                                                                                                                                                                                                                                                                            Query Match
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/note- "Xaa equals any amino acid residue or
amino acid residue"
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/note- "Xaa equals any amino acid residue or
amino acid residue"
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/note= "Xaa equals any amino acid residue or
amino acid residue"
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/note- "Xaa equals any amino acid residue
amino acid residue"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              any amino acid residue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /label- Unknown
/note- "Xaa equals
amino acid residue"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     label- Unknown
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             label- Unknown
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                                                                                                                                                                                                                          Misc-difference 118
                                                                                                                                                                                                                                                                                                                                     Misc-difference 159
                                                                                                             Misc-difference 108
                                                                                                                                                                                                                                                    Misc-difference 122
                                                                                                                                       Misc-difference 111
Misc-difference 62
                                                                                                                                                                                                                                                                               Misc-difference 12
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                           Misc-difference 79
                                                                                                                                                                  Misc-difference 13
                                                                                 Misc-difference 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ruben SM, Ni J;
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1;

Gaps

ABG33910 standard; Protein; 148 AA.

RESULT 9 ABG33910 ABG33910;

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AAD11630-AAD11721 represent cDNAs corresponding to 71 human secreted
protein genes, and AAE06041-AAE06132 represent the proteins they encode.

AEA06133-AAE06505 represent human secreted protein they encode.
The secreted proteins and their genes are useful for preventing, treating
or ameliorating medical conditions, e.g., by protein or gene therapy.
The secreted proteins can be diagnosed by determining the amount of the
new protein in a sample or by determining the presence of mutations in
the new genes. Specific uses are described for each of the 71 genes,
based on the tissues in which they are most highly expressed, and include
developing products for the diagnosis or treatment of proliferative
disorders, cancer, tumours, foetal and developmental abnormalities,
haematopoietic disorders, diseases of the immune system, AIDS, autoimmune
diseases (e.g., rheumanatoid arthritis), inflammation, allergies,
cognitive disorders (e.g., Alzheimer's disease, Parkinson's disease),
cognitive disorders, schizophrenia, asthma, skin disorders (e.g.,
prognancy-related disorders, and electrons. The
proteins can also be used to aid wound healing and epithelial cell
proteins can also be used to aid wound healing and epithelial cell
proteins can also be used to aid wound healing and epithelial cell
proteins are also be used to aid wound healing and epithelial cell
proteins can also be used to aid wound healing and epithelial cell
proliferation, to prevent skin aging due to sunburn, to maintain organs
controlled the process of the process of the profession of primary tissues,
controlled the process of the controlled to the process of th
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                                                                                                                                                                                                                                                                                                                                              Shi Y;
Soppet DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          55 --APRRFRRSVPR-GEAAGAVQELARALAHLLEAERQERARAEAQEAEDQQARVLAQLLR 111
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Isolated nucleic acid molecule encoding a human secreted protein is used in preventing, treating or ameliorating a medical condition
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MAGSPLLWGPRAGGVGLLVLLLGLFRPPPALCARPVKEPRGLSAASPPLAETG-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MAGSPLLWGPRAGGVGLLVLLLLGLFRPPPALCARPVKEPRGLSAASPPLARLALLAASG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SPISKRASW----RSCCASG-----APPATLIRLWAWTTTPTRLQRSSLALCSAPA 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   112 V----WGAPRNSDPALGLDDDPDAPAQLAR----ALLRARLDPAALAAQLVPA 157
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                                                                                                                                                                                                                                                                                                                                                 Moore PA, S
Young PE,
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34..148
/label= Mature_human_secreted_protein
                                                                                                                                                                                                                                                                                                                                           Ruben SM, Kómatsoulis GA, Duan DR, Rosen CA, P
Lafleur DW, Olsen HS, Brewer LA, Florence KA,
Endress GA, Muscenski M, Ebner R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 11; Page 773-774; 864pp; English.
                                                                                                                                                                                                                                                                                            (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                   12-JAN-2001; 2001WO-US00911.
                                                                                                                                                                                                                                        13-JAN-2000; 2000US-0482273.
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Best Local Similarity
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                                                                             WO200151504-A1
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fragment, homologue complement or allelic variant) encoding a human secreted protein (and its fragment, domain, epitope, variant, secreted fragment, homologue complement or allelic variant) encoding a human secreted protein (and its fragment, domain, epitope, variant, secreted form and species variant). Also included are a recombinant vector comprising the nucleic acid, a recombinant host cell comprising the vector, an antibody against the secreted protein, a recombinant host cell that expresses the secreted protein and method of identifying a binding partner of the secreted protein and method of identifying a binding partner of the secreted protein and method of identifying a binding partner of the secreted protein. The nucleic acid and protein are used to prevent, diagnose, treat or ameliorate a medical condition in e.g. prevent, abblist, goats, horses, cats, dogs, chickens or sheep for example autoimmune diseases e.g. rheumatoid arthritis, hyperproliferative disorders e.g. neoplasms of the breast or liver, cardiovascular disorders e.g. cardiac arrest, cerebrovascular disorders e.g. cardiac arrest, cerebrovascular disorders e.g. cardiac arrest, cerebrovascular disorders e.g. corneal infection. Many other diseases and disorders are listed in the specification. The polypeptides can also be used to aid wound healing an epithalial cell proliferation, to prevent skin aging due to sunburn, to maintain organs before transplantation, for supporting cell culture of primary tissues, to regenerate tissues and in chemotaxia. The polypeptides can also be used as a food additive or preservative to increase or decrease storage capabilities. The present sequence represents a novel human secreted protein of the invention.
                                                                                                                            Human; secreted protein; gene therapy; immunosuppressive; antirheumatic; antiproliferative; cytostatic; cardiant; vasotropic; cerebroprotective; notropic; neuroprotective; antibacterial; virucide; fungicide; opthalmalogical; autoimmune disease; neoplasm; rheumatoid arthritis; hyperproliferative disorder; cardiac arrest; cardiovascular disorder; cerebral ischaemia; angiogenesis; nervous system disorder; Alzheimer's disease; infection; coular disorder; corneal infection; wound healing; skin aging; epithelial cell proliferation; food additive.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel 71 isolated secreted polypeptides and polynucleotides encoding the polypeptides, useful for treating Huntington's disease, sepsis, meningitis, thrombocytopaenia, haemolytic anaemia, rheumatoid arthritis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Shi Y;
Soppet DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Moore PA,
Young PE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Duan DR, Rosen CA,
Wer LA, Florence KA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 11; Page 1252-1253; 1478pp; English.
                                                                                    Human secreted protein encode by gene 48.
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Komatsoulis G, Dua...
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                                            (first entry)
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Endress GA, Mucenski M,
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N-PSDB; ABK69773.
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                                                                                                                                                                                                                                                                                                                                                               Homo sapiens.
                                          15-JUL-2002
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148 AA;

Sequence

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Lafleur DW,
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                                                                                                                                                                                                                                                                                                                                                            antinflammatory; nootropic; neuroprotective; antiallergic; cancer; tumour; neurodegenerative disorder; developmental abnormality; allergy; foetal deficiency; blood disorder; immune system disorder; arthritis; autoimmune disease; hepatic disease; renal disease; inflammation; Alzheimer's disease; behavioural disorder; schizophrenia; osteoporosis; infection; AlDS; spinal cord injury; transplant rejection; diabetes; asthma; sepsis, acne; psoriasis; cardiovascular disorder; disorder; pastrointestinal disorder; respiratory disorder; metabolic disorder; food additive; preservative.
                                                                                                            55 --APRRFRRSVPR-GEAAGAVQELARALAHLLEAERQERARAEAQEAEDQQARVLAQLLR 111
                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Young PE;
                                                                       secreted protein; diagnosis; cytostatic; immunosuppressive;
                                                          1 MAGSPLLWGPRAGGVGLLVLLLGLFRPPPALCARPVKEPRGLSAASPPLAETG-----
                                                                                                                           Shi Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New isolated human genes, useful for diagnosis and treatment of, cancers, neurological or blood disorders
                                                                                                                                                          112 V----WGAPRNSDPALGLDDDPDAPAQLAR----ALLRARLDPAALAAQLVPA 157
                                                                                                                                                                                   99 ISRRASW----RSCCASG-----APPATLIRLWAWITIPITRLORSSLALCSAPA 143
                                    50;
           Length 148;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Komatsoulis G, Duan RD, Rosen CA, Moore PA,
Ebner R, Olsen HS, Brewer LA, Florence KA,
Endress GA, Soppet DR;
                                   34; Indels
         Score 308; DB 23;
Pred. No. 1.4e-18;
                                                                                                                                                                                                                                                                                                                           Human secreted protein sequence SEQ ID NO:150.
                                 3; Mismatches
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                                                                                                                                                                                                                                                AAY87111 standard; Protein; 149 AA
          23.4%;
50.3%;
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98US-0092956.
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                                   88; Conservative
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         Query Match
Best Local Similarity
Matches 88; Conserv
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15-JUL-1998;
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Mucenski M,
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can be diagnosed by determining the amount of the new polypeptides in a sample or by determining the presence of mutations in the new polydedides. Human secreted protein s and their polynucleotides can be used for developing products for the diagnosis or treatment of cancer, tumours, neurodegenerative disorders, developmental abnormalities and foetal deficiencies, blood disorders, diseases of the immune system, autoimmune diseases, hepatic and renal disease, inflammation, allergies, Alzheimer's disease, behavioural disorders, schizophrenia, osteoporosis, arthritis, infections, ADS, spinal cord injuries, transplant rejection, diabetes, asthma, sepsis, acne, psoriasis, cardiovascular disorders, reproductive disorders, gastrointestinal disorders, respiratory disorders and metabolic disorders. The cardiovascular disorders and metabolic disorders. The proteins are also useful for identifying their binding partners. AAZ298008 to AAZ98008 and AAX87063 are sequence used in the exemplification of the present invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              reproductive disorder; gastrointestinal disorder; respiratory disorder; metabolic disorder; food additive; preservative.
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Young PE;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 GQCPEVRRGRCRPGAGAGA-----SAGAERQERARAEAQR-----LR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  112 V----WGAPRNSDPALGLDDDPDAPAQLAR----ALLRARLDPAALAAQLVPA 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99 ISRRASW----RSCCASG-----APPATLIRLWAWITIPIRLQRSSLALCSAPA 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 308; DB 21; Length 149;
Pred. No. 1.4e-18;
3; Mismatches 34; Indels 50;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Komatsoulis G, Duan RD, Rosen CA, Moore PA,
Ebner R, Olsen HS, Brewer LA, Florence KA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human secreted protein sequence SEQ ID NO:238.
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98US-0092922.
98US-0092956.
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50.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       88; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 88; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       149 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO200004140-A1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                09-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15-JUL-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5-JUL-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15-JUL-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     27-JAN-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ruben SM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 11
AAY87199
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The polynucleotide sequences given in AA298017 to AA298108 encode the human secreted proteins given in AAY87064 to AAY87223. Human secreted proteins given in AAY87064 to AAX87223. Human secreted protein can have activities based on the tissues and cells the genes are expressed in. Examples of activities include: cytostatic; immunosuppressive; antiniflammatory; nootropic; neuroprotective; and antialized; or the polynucleotides and their corresponding secreted polypeptides are useful for preventing, treating or ameliorating medical polypeptides are useful for preventing, treating or ameliorating medical conditions, e.g. by protein or gene therapy. Also pathological conditions can be diagnosed by determining the amount of the new polypeptides in a sample or by determining the proteins and their polynucleotides can can be diagnosed by determining the amount of the new polypeptides in a sample or by determining products for the diagnosis or treatment of cancer, tumours, neurodegenerative disorders, diseases of the immune system, autoimmune diseases, boad disorders, diseases of the immune system, allergies, Alzheimer's disease, behavioural disorders, schizophrenia, cartoimmune diseases, behavioural disorders, schizophrenia, cardiovascular disorders asthma, sepsis, acne, psoriasis, cardiovascular disorders and metabolic disorders. The proteins are also used as food additives or proteins or polynucleotides can also be used as food additives or proteins are also used also defined binding partners. AA298008 to AA298016 and AAX87063 are sequence used in exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  foetal abnormality; developmental abnormality; haematopoletic disorder; immune system disorder; ALDS; autoimmune disease; rheumatoid arthritis; Parkinson's disease; cognitive disorder; schizophrenia; skin disorder; psoriasis; sepsis, diabetes; atherosclerosis; cardiovascular disorder; inflammation; neurological disorder; Alzheimer's disease; food additive; anglogenic disorder; klacker; allergy; pregnancy related disorder; endocrine disorder; allergy; pregnancy related disorder; endocrine disorder; allergy; cell culture; chemotaxis; vulnerary; binding partner identification;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               secreted protein; proliferative disorder; cancer; tumour; asthma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            79 GOCPEVRRRGRCRPGAGAGA-----SAGAERQERARAEAQR-----LR 116
                                                                                                                   New isolated human genes, useful for diagnosis and treatment of, e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             --APRRFRRSVPR-GEAAGAVQELARALAHLLEAERQERARAEAQEAEDQQARVLAQLLR 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MAGSPLLWGPRAGGVGLLVLLLLGLFRPPPALCARPVKEPRGLSAASPPLAETG----- 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        19 MAGSPLLWGPRAGGVGLLVLLLLGLFRPPPALCARPVKEPRGLSAASPPLARLALLAASG 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              112 V----WGAPRNSDPALGLDDDPDAPAQLAR----ALLRARLDPAALAAQLVPA 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          117 ISRRASW----RSCCASG-----APPATLIRLWAWTTTPTRLORSSLALCSAPA 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human gene 48 encoded secreted protein fragment, SEQ ID NO:238.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       34; Indels 50;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 308; DB 21; Length 166;
Pred. No. 1.6e-18;
3; Mismatches 34; Indels 50
                                                                                                                                                     cancers, neurological or blood disorders
                                                                                                                                                                                               Disclosure; Page 470; 494pp; English.
  Soppet DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAE06176 standard; Protein; 166 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23.4%;
50.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            24-SEP-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     88; Conservative
  Endress GA,
                                               WPI; 2000-161128/14.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    166 AA;
                                                                      N-PSDB; AAZ98064
Mucenski M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
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AAE06176
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protein of the invention can be used in alleviating symptoms associated with the disorders mentioned above, and in diagnostic immunoassays e.g., radioimmunoassay or enzyme linked immunosorbent assay (ELISA).
                                                                                                                                                                                Soppet DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                before transplantation, for supporting cell culture of primary tissues, to regenerate tissues, to identify their cognate ligands or binding partners, and in chemotaxis, and can be used as a food additive or preservative to modify storage properties. Antibodies specific for a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             55 --APRRFRRSVPR-GEAAGAVQELARALAHLLEAERQERARAEAQEAEDQQARVLAQLLR 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          19 MAGSPLIMGPRAGGVGLLVLLILGLFRPPPALCARPVKEPRGLSAASPPLARLALLAASG 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MAGSPILLWGPRAGGVGLLVLLLLGLFRPPPALCARPVKEPRGLSAASPPLAETG----- 54
                                                                                                                                                                                                                                          Isolated nucleic acid molecule encoding a human secreted protein is
                                                                                                                                                                     Shi Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   79 GQCPEVRRRGRCRPGAGAGA-----SAGAERQERARAEAQR-----LR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present sequence represents a human secreted protein fragment
                                                                                                                                                                                                                                                       used in preventing, treating or ameliorating a medical condition
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           112 V----WGAPRNSDPALGLDDDPDAPAQLAR----ALLRARLDPAALAAQLVPA 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           34; Indels 50;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 166;
                                                                                                                                                                                 Young PE,
                                                                                                                                                                     Moore PA,
                                                                                                                                                                 Komatsoulis GA, Duan DR, Rosen CA,
Olsen HS, Brewer LA, Florence KA,
Muscenski M, Ebner R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 308; DB 22;
Pred. No. 1.6e-18;
3; Mismatches 34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                referred to in the disclosure of the invention.
                                                                                                                                                                                                                                                                             Disclosure; Page 122; 864pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23.4%;
50.3%;
                                                                                                                                             (HUMA-) HUMAN GENOME SCI INC
                                                                                             12-JAN-2001; 2001WO-US00911.
                                                                                                                    13-JAN-2000; 2000US-0482273.
                                                                                                                                                                                         Endress GA, Muscenski M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                  WPI; 2001-425865/45.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 88; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 166 AA;
                                             WO200151504-A1.
                       Homo sapiens.
gene therapy.
                                                                                                                                                                                Lafleur DW,
                                                                     19-JUL-2001
                                                                                                                                                                   Ruben SM,
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Length 166;

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Human; secreted protein; gene therapy; Immunosuppressive; antitheumatic; antiproliferative; cytostatic; cardiant; vasotropic; cerebroprotective; nootropic; neuroprotective; antibacterial; virucide; fungicide; opthalmalogical; autoimmune disease; neoplasm; rheumatoid arthritis; hyperproliferative disorder; cardiac arrest; cardiovascular disorder; cerebral ischaemia; angiogenesis; nervous system disorder; Alzheimer's disease; infection; ocular disorder; corneal infection; wound healing; skin aging; epithelial cell proliferation; food additive.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel 71 isolated secreted polypeptides and polynucleotides encoding the polypeptides, useful for treating Huntington's disease, sepsis, meningitis, thrombocytopaenia, haemolytic anaemia, rheumatoid arthritis,
                                                                                                                                                                                                                                                                                                                                                                                Lafleur DW, Olsen H, Brewer LA, Florence KA, Woore PA, Shi Y;
Endress GA, Mucenski M, Ebner R;
                                                                                  Human secreted protein #2 encoded by gene 48.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Page 1316-1317; 1478pp; English.
           ABG34000 standard; Protein; 166 AA.
                                                                                                                                                                                                                                                                                                                                                                  (HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                                                                                                                                                                                               25-SEP-2000; 2000US-234925P. 12-JAN-2001; 2001WO-US00911.
                                                                                                                                                                                                                                                                                                      24-SEP-2001; 2001WO-US29871.
                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2002-362489/39.
N-PSDB; ABK69773.
                                                                                                                                                                                                                                                       WO200226931-A2
                                                                                                                                                                                                                                Homo saptens.
                                                          15-JUL-2002
                                                                                                                                                                                                                                                                               04-APR-2002.
                                   ABG34000;
ABG34000
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fragment, homologue complement or allelic variant) encoding a human secreted protein (and its fragment, domain, epitope, variant, secreted fragment, homologue complement or allelic variant) encoding a human secreted protein (and its fragment, domain, epitope, variant, secreted comprising the nucleic as variant). Also included are a recombinant vector comprising the nucleic acid, a recombinant host cell comprising the vector, an antibody against the secreted protein are arecombinant host cell that expresses the secreted protein and a method of identifying a binding partner of the secreted protein. The nucleic acid and protein are used to prevent, diagnose, treat or ameliotate a medical condition in e.g. prevent, diagnose, treat or ameliotate a medical condition in e.g. for example autoimmune diseases e.g. rheumatoid arthritis, clore example autoimmune diseases e.g. rheumatoid arthritis, chyperproliferative disorders e.g. rheumatoid arthritis, cardiovascular disorders e.g. cardiac arrest, cerebrovascular disorders e.g. cardiac arrest, cerebrovascular disorders e.g. corneal infection. Many other diseases and in clasorders are listed in the specification. The polypeptides can also be used to aid wound healing an epithalial cell proliferation, to prevent cused to aid wound healing an epithalial cell proliferation, to regenerate tissues and in chanctaris. The polypeptides can also be used as a food additive chanctaris. The polypeptides can also be used as a food additive chanctaris. The polypeptides can also be used as a food additive chance represents a novel human secreted protein of the invention. invention relates to an isolated nucleic acid molecule (or its

diseases.

166 AA;

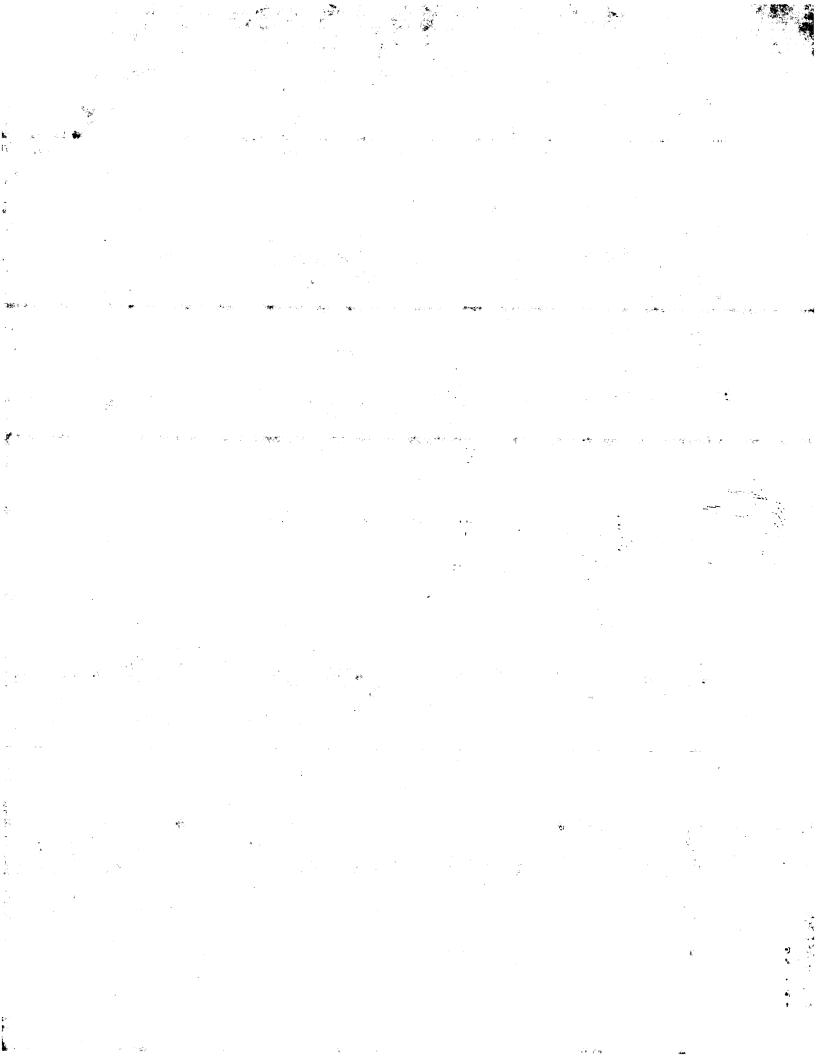
Sequence

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The present sequence is a rat pituitary hormone, pituitrone.

Pituitrone is highly expressed in pituitary gland and is also expressed in pituitary gland and is also expressed in prain tissues, spinal cord and kidney. It may be used as antigens in the production of antibodies against pituitrone and in assays to identify modulators. Pituitrone cDNAs are also useful in gene therapy. Pituitrone may be used in the prevention, treatment and diagnosis of diseases associated with inappropriate pituitrone expression. It may be useful in treating disorders related to reproductive and renal system, immune disorders, disorders of the controlls (e.g., aneamia, ingreders, blood coagulation disorders, autolumune disorders (e.g. addisorders) blood coagulation clisorders, autolumune disorders (e.g. addisorders (SLE)), hyperproliferative disorders (e.g. neoplasms of bone, liver and pancreas) and infectious
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Digeoige syndrome; haematopoietic cell; ataxia telangiectasia; Wiskott-Aldrich disorder; blood coagulation disorder; Addison's disease; autoimmune disorder; multiple sclerosis; systemic lupus erythematosus; SLE; hyperproliferative disorder; gene therapy; neoplasm; infectious disease; immunomodulatory; cytostatic; antimicrobial.
                                                                                                                                                          --APRRFRRSVPR-GEAAGAVQELARALAHLLEAERQERARAEAQEAEDQQARVLAQLLR 111
                                                                                                                                                                                               Nucleic acids encoding a novel pituitary hormone (pituitrone), useful
                                          Gaps
                                                                               54
                                                                                                                 19 MAGSPLLWGPRAGGVGLLVLLLGLFRPPPALCARPVKEPRGLSAASPPLARLALLAASG 78
                                                                             1 MAGSPLLWGPRAGGVGLLVLLLLGLFRPPPALCARPVKEPRGLSAASPPLAETG----
                                                                                                                                                                                                                                                            112 V----WGAPRNSDPALGLDDDPDAPAQLAR----ALLRARLDPAALAAQLVPA 157
                                        50;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             for diagnosing, preventing and treating e.g. immune disorders, hyperproliferative disorders and blood coagulation disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rat; pituitary; pituitrone; therapy; immune disorder; anaemia;
                                        Indels
Query Match 23.4%; Score 308; DB 23; Best Local Similarity 50.3%; Pred. No. 1.6e-18; Matches 88; Conservative 3; Mismatches 34.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rat pituitary hormone, pituitrone.
                                                                                                                                                                                                                                                                                                                                                                          AAY71961 standard; Protein; 69 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 11; Fig 2; 277pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (HUMA-) HUMAN GENOME SCI INC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99US-0131966
                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO200066778-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     26-MAR-2001
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                                                                                                                                                                                                                                                                                                                                                                                                              AAY71961;
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Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention describes a recombinant protein (I) from a lymphoma associated protein (LAP) sequence of Pik3r1, GNAS (including associated protein (LAP) sequence of Pik3r1, GNAS (including to a second to a bioactive agent capable of binding to an LA protein (LAP) which is encoded by a polynucleotide (II) and (II) is useful for evaluating the effect of a candidate lymphoma drug in a patient. (I) and (II) is also useful for diagnosing lymphoma involving determining the expression of one or more (II), or (I) encoded by (II) in a first tissue type of a first individual and comparing the expression of the gene(s) from a second normal tissue type from the first individual or a second unaffected individual, where a difference in the expression indicates that the first individual has lymphoma. (II) is useful in the comprising (II) is useful for screening drug candidates which involves providing the host cell that expresses LA gene, adding a drug candidate on the contract.
                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                 Lymphoma associated protein; Pik3rl; GNAS; XI_(alpha_s_); NESP55; JAKl; Neurogranin; Nfr2; lymphoma; DNA vaccine; cytotoxic T-cell; animal model; leukaemia.
                                                                                                        193 ELLRYLLGRILAGSADSEGVAAPRRLRRAADHDVGSELPPEGVLGALLRVKRLETPAPQV 252
                                                                           Gaps
                                                                                                                        2 ELLRYLLGRILTGSSEPEAAPAPRILRAVDQDLGPEVPPENVLGALLRVKRLENSSPQA 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        expression of the LA gene. LA genes are also administered as DNA vaccines, such that expression of the polypeptide encoded by the DNA
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                                              Length 69;
                                           Score 259; DB 21; Length 6
Pred. No. 8.2e-15;
5; Mismatches 12; Indels
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                                                                                                                                                                                                                                                                            ABG60300 standard; Protein; 388 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2000US-0668644.
2001US-0905390.
2001US-0905491.
                                           Query Match 19.6%;
Best Local Similarity 75.0%;
Matches 51; Conservative
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                                                                                                                                                                   253 PARRLLPP 260
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|PARRLLPP 69
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13-JUL-2001;
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vaccine, cytotoxic T-cells and antibodies are induced which recognise and destroy or eliminate cells expressing LA proteins. The genes are also for generating animal models of lymphoma. This sequence represents a lymphona associated protein described in the invention.
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receptor; specific binding agent; probe; primer; hybridisation;
amplification; mutation; genetic mapping; ss.
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/product= "Tango-81"
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           GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
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GAGGCAGGCGACGAGACCCCGACGTGGACCCCGAGCTGTTGAGGTACTTGCTGGGACGG
               ATTCTTGCGGGAAGCGCGGACTCCGAGGGGGTGGCAGCCCCGCGCCGCCGCTCCGCCGTGCC
                                                           GTGAAACGCCTAGAGACCCCGGCGCCCCAGGTGCCTGCACGCCGCCTCTTGCCACCCTGA
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P-PSDB; AAM39005.
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Zhao QA,
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                                                                                                               protein used in the method of the invention. Host cells containing the Tango protein are used to produce recombinant proteins for raising antibodies. It is also used in identifying specific binding agents (including cognate receptors), which can be used to determine amounts of recombinant protein in cells or the rapeutifally. Antibodies or other specific binding agents, are used to detect recombinant protein and fragments of the Tango concledes sequence can be used as probes or primers for detecting the Tango gene, specifically mRNA, in usual hybridisation or amplification assays. These assays are used for diagnosis of diseases associated with abnormal expression of Tango proteins, e.g. detecting mutations in the Tango genet; reagments of the Tango conclede aguence are also used for genetic mapping and chromosome identification, and as antisense, ribozyme or tribiar-furning therapeutics. Antibodies may also be used to generate
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                                                                                                                                                                                                                                                                                                                                            DB 20; Length 979;
                                                                                                        This is the nucleotide sequence encoding the human Tango-81
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100.0%; Pred. No. 0;
ive 0; Mismatches
                                                                                Claim 1; Fig 3; 67pp; English.
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Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer; peripheral nervous system; neuropathy; central nervous system; CNS; Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic; amyotrophic lateral sclerosls; Shy-Drager Syndrome; chemotactic; chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel nucleic acids and polypeptides, useful for treating disorders
                                                                                                                                                                                                                                                                                                                                                                                                      Ren F,
Zhang
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Yanq Y,
                                                                                                                                                                                                                                                                                                                                                                                                                 Yang
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Xu C, Xue AJ,
, Drmanac RT;
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                                                                     polynucleotide SEQ ID NO 364.
ВР
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Goodrich R,
                                                                                                                                                                                                                                                                   21-JAN-2000; 2000US-0488725.
25-APR-2000; 2000US-0552317.
9-JUL-2000; 2000US-0598042.
19-JUL-2000; 2000US-0653450.
14-SEP-2000; 2000US-0653450.
14-SEP-2000; 2000US-0653450.
19-OCT-2000; 2000US-0633134.
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Wang J, Wang Z, Wehrman T,
Zhao QA, Zhou P, Goodrich
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                                             (first entry)
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system, such as peripheral nervous injuries, peripheral neuropathy and
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09-JUL-2000;
19-JUL-2000;
03-AUG-2000;
14-SEP-2000;
19-OCT-2000;
29-NOV-2000;
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CC the encoded polypeptides (AAM38642-AAM42213) with notropic.

Immunosuppressant and cytostatic activity. The polynucleotides are useful

CC in gene therapy. A composition containing a polypeptide or polynucleotide

CC of the invention may be used to treat diseases of the peripheral nervous

CC system, such as peripheral nervous injuries, peripheral nervous to coalised neuropathy and

CC alzheimer's, Parkinson's disease, Huntington's diseases, such as

CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic

CC altisation of the activities such as: Immune system suppression,

CC and thrombolytic activity, cancer diagnosis and therapy, drug screening,

SC Alsorders.

CN A disorders.

CN A disorders.
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Pred. No. 0;
0; Mismatches
                                             Claim 1; SEQ ID NO 364; 10078pp; English.
  system injuries
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  nervous
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The invention relates to human nucleic acids (AAI57798-AAI61369) and the encoded polypeptides (AAM38642-AAM42213) with nootropic, limmunosuppressant and cytostatic activity. The polynucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ä
713 CCCCGCGCCCCCCCCCCCCCCCCCCCCACGATGTGGGCTCTGAGCTGCCCCCTGAGG 772
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                                                         GCGTGCTGGGGGGCGCTGCTGCGTGTGAACGCCTAGAGACCCCGGCGCCCCCAGGTGCCTG
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Zhang J;
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Yang Y,
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Wehrman T, Xu C, Xue AJ,
Goodrich R, Drmanac RT;
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Wang Z, Wehrman T, Xu C,
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ID AA159947 standard; cDNA; 1041
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2000US-0552317.
2000US-0598042.
2000US-0620312.
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2000US-0693036.
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localised neuropathles and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activities such as: Immune system suppression, Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, cancer diagnosis and therapy, drug screening, assays for receptor activity, arthritis and inflammation, leukaemias and C.N.S disorders.
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                                                                                              Score 891; DB 22; Length 1041;
Pred. No. 0;
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                                                                                 Sequence 1041 BP; 145 A; 356 C; 402 G; 138 T; 0 other;
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Matches 941;
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The invention relates to human nucleic acids (AAI57798-AAI61369) and the encoded polypeptides (AAM38642-AAM42213) with nootropic, immunosuppressant and cytostatic activity. The polynucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activities such as: Immune system suppression, Activin/inhibin activity, cancer disensels and thrombolytic activity, arthritis and inflammation, leukaemias and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  assays for receptor activity, arthritis and inflammation, leukaemias and C.N.S disorders.
Note: The sequence data for this patent did not form part of the printed specification.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer peripheral nervous system; neuropathy; central nervous system; CNS; Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic; amyotrophic lateral sclerosis; Shy-brager Syndrome; chemotactic; chemotactic; chemotactic; chemotactic; chemotactic; chemotactic; arthritis; inflammation;
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                            141 TGCCCCGCCATCCCGCCACCAGGACTGCTCCCGCCAGCACGTCCAGAGCAACTTACCC
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Zhang J;
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Yang Y,
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Xue AJ,
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Wehrman T, Xu
Goodrich R,
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ID AAI59948 standard; cDNA; 1041
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2000US-055317.
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2000US-0653450.
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Wang Z, Wi
Zhou P,
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14-SEP-2000;
19-OCT-2000;
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Wang J, W
Zhao QA,
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        BP; 145 A; 356 C; 402 G; 138 T; 0 other;
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                           DB 22;
                         Score 891; DB
Pred. No. 0;
0; Mismatches
                           91.0%;
99.9%;
                          Query Match 91.0
Best Local Similarity 99.9
Matches 941; Conservative
        Sequence 1041
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The present sequence is a cDNA clone HKGDL36 encoding human pituitary hormone, pituitrone. Pituitrone is highly expressed in pituitary gland and is also expressed in brain tissues, spinal cord and kidney. It may be used as antigens in the production of antibodies against pituitrone and in assays to identify modulators. Pituitrone and in seasys to identify modulators. Pituitrone cDNAs are also useful in gene therapy. Pituitrone may be used in the prevention, treatment and diagnosis of diseases associated with inappropriate pituitrone expression. It may be useful in treating disorders related to reproductive and renal system, immune disorders, disorders of haematopoietic cells (e.g., aneama, blgeorge syndrome, ataxia telangiectasia and Wiskott-Aldrich disorder), blood coagulation disorders, autoimmune disorders (e.g. Addison's disease, multiple sclerosis and systemic lupus extyhematosus (SLE)), hyperproliferative disorders (e.g. neoplasms of bone, liver and pancreas) and infectious
                                                                                                                                  Digeorge syndrome; haematopoietic cell; ataxia telangiectasia; wiskott-Aldrich disorder; blood coagulation disorder; Addison's disease; autoimmune disorder; multiple sclerosis; systemic lupus erythematosus; SLE; hyperproliferative disorder; gene therapy; neoplasm; infectious disease; immunomodulatory; cytostatic; antimicrobial; ss.
                                                                                                                                                                                                                                                                                                                                                                                                          /product- "Mature human pituitary hormone, pituitrone"
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                                                                                                                    immune disorder; anaemia;
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                                                                                                                                                                                                                                                                                                                       "Human pituitary hormone, pituitrone"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nucleic acids encoding a novel pituitary hormone (pituitrone), for diagnosing, preventing and treating e.g. immune disorders, hyperproliferative disorders and blood coagulation disorders -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 21; Length 1043;
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                                                                                encoding human pituitary hormone, pituitrone.
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Pred. No. 0;
0; Mismatches
                                                                                                                    therapy;
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                                                                                                                    pitultary; pitultrone;
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Best Local Similarity 99.9%;
Matches 941; Conservative
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S RESULT healing;

hydrophobic domain; immunosuppressant; anti-HIV; neuroprotective;

antianaemic; vulnerary; antiuloer; osteopathic; anti-inflammatory; cytostatic; gene therapy; autoimmune disorder; multiple sclerosis; HIV infection; anaemia; burn; ulcer; osteoporosis; tumour; wound healuinflammatory bowel disease; nutritional supplement; appetite; vaccine; behavioural characteristic; immune response; ss.

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Human proteins with hydrophobic domains and the DNAs which encode them are useful for treating autoimmune disorders, burns and tumors and for

(SAGA ) SAGAMI CHEM RES CENT (PROT-) PROTEGENE INC.

Kimura T;

ŝ Kato WPI; 2001-160059/16. P-PSDB; AAB88596.

99JP-0252551. 99JP-0301624.

07-SEP-1999; 01-OCT-1999; 22-OCT-1999; 04-NOV-1999;

17-AUG-1999

2000WO-JP05356 99JP-0230344

10-AUG-2000;

22-FEB-2001

WO200112660-A2. Homo sapiens.

Claim 4; Page 461-463; 518pp; English. screening novel pharmaceuticals -

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AXE AAF9417 to AAF94516 encode the human proteins given in AAB88557 to AAB88606 (I) which have a hydrophobic domain. (I) have immunosuppressant, anti-inflammatory and cytostatic activities, and can be costeopathic, anti-inflammatory and cytostatic activities, and can be used in gene therapy. (I) can be used as pharmaceuticals and as antigens to prepare antibodies. DNA and cDNA (II) encoding (I) can be used as producing (I) in large quantities. Cells containing (II) are used for producing (I) in large quantities. Cells containing (II) are used for the detection of ligands or receptors corresponding to membrane or secretory proteins and to screen small molecule novel pharmaceuticals. Chilbodies directed to (I) can be used for the detection, quantification and printification of (I). Activities of (I) may include cytokine and cell proliferation/differentiation function, immune stimulating or suppressing activity, haematopolesis regulating activity, tissue growth activity, activity, nematopolesis regulating activity, tissue growth activity, activity, and (II) can be used to treat autoimmune disorders e.g. multiple sclerosis, HIV infections, anaemia, burns, ulcers, osteoporosis, continuametory bowel disease and tumours. (I) and (II) can also be used for carbon or nitrogen source, to effect metabolism, carbohidam, anabolism, carbon or nitrogen source, to effect metabolism, carbohidam and unimune as an and an and act as antigens in vaccines to raise an immune response to the protein or another material cross-reactive with the protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30 GCCCGGCTCGCTGGGGCACGATGGCGGGGTCGCCCCTCTGGGGGGCCCCGGGGG 89
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Indels

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04-JUN-2001 AAF94496;

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AAF94496

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Human; hydrophobic domain; immunosuppressant; anti-HIV; neuroprotective;
antianaemic; vulnerary; antiulcer; osteopathic; anti-inflammatory;
cytostatic; gene therapy; autoimmune disorder; multiple sclerosis;
HIV infection; anaemia; burn; ulcer; osteoporosis; tumour; wound healing;
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Human hydrophobic domain containing protein clone HP10756 cDNA #110
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                              AGGCGCAGGAGGCTGAGGATCAGCAGGCGCGCTCCTGGCGCAGCTGCTGCTCGCGTCTGGG
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                    CGCGGCCGGTAAAGGAGCCCCGCGGCCTAAGCGCAGCGTCTCCGCCCTTGGCTGAGACTG
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AC AAF9
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DT 04-J
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                                                                                                                                                                                               Human proteins with hydrophobic domains and the DNAs which encode them are useful for treating autoimmune disorders, burns and tumors and for screening novel pharmaceuticals -
inflammatory bowel disease; nutritional supplement; appetite; vaccine; behavioural characteristic; immune response; ss.
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                                                                                                                                                                                                                              Claim 3; Page 431-432; 518pp; English.
                                                                                   99JP-0230344.
99JP-0252551.
99JP-0281132.
99JP-0301624.
                                                                                                                                   CHEM RES CENT
                                                                    2000WO-JP05356
                                                                                                                   99JP-0313877
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Matches 778; Conservative
                                                                                                                                  (SAGA ) SAGAMI CHEM RE
(PROT-) PROTEGENE INC.
                                                                                                                                                                       WPI; 2001-160059/16.
P-PSDB; AAB88596.
                                                                                                                                                         Kato S, Kimura T;
                                      WO200112660-A2
                       Homo sapiens.
                                                                    10-AUG-2000;
                                                                                  17-AUG-1999;
07-SEP-1999;
01-OCT-1999;
22-OCT-1999;
04-NOV-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; secreted protein; diagnosis; cytostatic; immunosuppressive; antidifammatory; nootropic; neuroprotective; antiallergic; cancer; tumour; neurodegenerative disorder; developmental abnormality; allergy; foetal defliciency; blood disorder; immune system disorder; arthritis; autoimmune disease; hepatic disease; renal disease; inflammation; allahencis adisease; behavioural disorder; schizophrenia; osteoporosis; infection; AIDS; spinal cord injury; transplant rejection; diabetes; asthma; sepais; acne; psoriasis; cardiovascular disorder; respiratory disorder; respiratory disorder;
                                                                                                                                                            477
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CGCGGCCTAAGCGCAGCGTCTCCGCCCTTGGCTGAGACTGGCGCTCCTCGCCGCTTCCGG 180
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                                   CATCTGCTGGAGGCCGAACGTCAGGAGCGGGCGGGGCGCGAGGCGGAGGCTGAGGAT
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                      GCGCGCGCCCCCGGCCCCCGGTCTACGACGACGCCCCGGGGCCCGGGATGCT
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The polynucleotide sequences given in AA298017 to AA298108 encode the human secreted proteins given in AA897064 to AAY87233 Human secreted proteins given in AA897064 to AAX87233 Human secreted proteins given in AA897064 to AAX87233 Human secreted protein can have activities based on the tissues and cells the genes are expressed in. Examples of activities include: cytostatic; immunosuppressive; antiinfalmmatory; nootropic; neuroprotective; and antiallargic. The polynucleotides and their corresponding secreted polypeptides are useful for preventing, treating or ameliorating medical conditions, e.g. by protein or gene therapy. Also pathological conditions can be diagnosed by determining the amount of the new polypeptides in a sample or by determining the presence of mutations in the new complete to developing products for the diagnosis or treatment of cancer, tumours, neurodegenerative disorders, developmental abnormalities and complement of entering and disorders blood disorders, diseases of the immune system, altergies, Alzheimer's disease, behavioural disorders, schizophrenia, catalorgies, Alzheimer's disease, behavioural disorders, schizophrenia, catalorgies, Alzheimer's disease, behavioural disorders, schizophrenia, cardiovascular disorders, reproductive disorders, gastrointestinal disorders, respiratory disorders and metabolic disorders. The proteins are also useful for identifying their the analytical completives or the proteins are also useful for identifying their the analytical completives.
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Young
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                                                                                                                                                                                                                                                        diagnosis and treatment of,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 1050;
                                                                                                     G, Duan RD, Rosen CA, Moore PA,
Olsen HS, Brewer LA, Florence KA,
1, Soppet DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 583; DB 21;
Pred. No. 3.1e-250;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      the exemplification of the present invention
                                                                                                                                                                                                                                                    New isolated human genes, useful for diac
cancers, neurological or blood disorders
                                                                                                                                                                                                                                                                                                                      Claim 1; Page 339; 494pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   59.6%;
                                                             (HUMA-) HUMAN GENOME SCI INC.
98US-0092922.
98US-0092956.
                                                                                                                           Ebner R, Ol
Endress GA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 99.8 Matches 633; Conservative
                                                                                                   Komatsoulis
                                                                                                                                                                                      WPI; 2000-161128/14.
                                                                                                                                                                                                              P-PSDB; AAY87111
                                                                                                                           DW,
                                                                                                                             Lafleur DW,
Mucenski M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local $
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706 GGCCTCCGCCGTGCCGCCGACCACGATGTGGGCTCTGAGCTGCCCCCTGAGGGCGTGCTG

98US-0092921.

15-JUL-1998;

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Human; secreted protein; proliferative disorder; cancer; tumour; asthma; foetal abnormality; developmental abnormality; heematopoietto disorder. Immune system disorder; AIDS; autoimmune disease; rheumatoid arthritis; Parkinson's disease; confitive disorder; schizophrenia; sin disorder; psoriasis; sepsis; diabetes; atherosclerosis; cardiovascular disorder; inflammation; neurological disorder; Alzheimer's disease; food additive; angiogenic disorder; kidney disorder; gastrointestinal disorder; allergy; pregnancy-related disorder; endocrine disorder; infection; wound healing; gene therapy; ss.
                                                                                                                                                                                                                                                                                                                                                   Human secreted protein-encoding gene 48 cDNA clone HKGDL36, SEQ ID NO:58.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Shi Y;
Soppet DR;
                                                                                                                                    945
                                      825
                                                             818
                                                                                      885
                                                                                                                                                 Isolated nucleic acid molecule encoding a human secreted protein is used in preventing, treating or ameliorating a medical condition
                                                                                  886 CCATCCGGCCACCAGGACTGCTCCCGGCCAGGACGTCCAGAGCAACTTACCCCGGGCCAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
55..501
/*tage a /
/product= "Human secreted protein precursor"
55..153
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Young PE,
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14..498
/*tag= c
/product= "Mature human secreted protein"
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Florence KA,
                                                                                                                                                                                                 939 CAGCCCTCTCACCCGAGGATCCCTACCCCCTGGC 972
                                                                                                                                                                                    946 CAGCCCTCTCACCCGAGGATCCCTACCCCTGGC 979
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Lafleur DW, Olsen HS, Brewer LA, F
Endress GA, Muscenski M, Ebner R;
                                                                                                                                                                                                                                                                        AAD11677 standard; cDNA; 1050 BP
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P-PSDB; AAE06088.
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AAD11630-AAD11721 represent CDNAs corresponding to 71 human secreted.

Crossista AAE06132 represent the proteins they encode.

AAE06133-AAE06205 represent human secreted protein fragments.

Crossista AAE06205 represent human secreted protein fragments.

Crossista AAE06133 represent the proteins they encode.

AE0613-AAE06205 represent human secreted protein fragments.

Crossista and their genes are useful for preventing, treating or ameliorating medical conditions, e.g., by protein or gene therapy.

Crossista and protein in a sample or by determining the presence of mutations in the new genes. Specific uses are described for each of the 71 genes, based on the tissues in which they are most highly expressed, and include developing products for the diagnosis or treatment of proliferative disorders, cancer, tumours, foetal and developmental abnormalities, haematopoietic disorders, diseases of the immune system, AIDS, autoimmune diseases (e.g., Alzheimer's disease, Parkinson's disease), cognitive disorders, schizophrenia, asthma, skin disorders (e.g., paoriasis), sepsis, diabetes, atherosclerosis, cardiovascular disorders, candiopenic disorders, independent disorders, madiophrenia, asthma, skin disorders, pregnancy-related disorders, endocrine disorders, and infections. The proteins can also be used to aid wound healing and epithelial cell corporate tissues, to identify their cognate ligands or binding to processes, and or percent skin adding the consular disorders, and consular disorders, corporate tissues, to identify their cognate ligands or binding to processes and consular disorders, consular disorders, and con
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               preservative to modify storage properties. Antibodies specific for a protein of the invention can be used in alleviating symptoms associated with the disorders mentioned above, and in diagnostic immunoassays e.g., radioimmunoassay or enzyme linked immunosorbent assay (ELISA).
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Claim 1; Page 706; 864pp; English.
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Matches 633; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            fragment, homologue complement or allelic variant) encoding a human secreted protein (and its fragment, domain, epitope, variant, secreted fordein (and its fragment, domain, epitope, variant, secreted form and species variant). Also included are a recombinant vector comprising the nucleic acid, a recombinant host cell comprising the vector, an antibody against the secreted protein, a recombinant host cell that expresses the secreted protein and a method of identifying a binding partner of the secreted protein. The nucleic acid and protein are used to prevent, diagnose, treat or ameliorate a medical condition in e.g. prevent, diagnose, treat or ameliorate a medical condition in e.g. prevent, arbbits, goats, horses, cats, dogs, chirkens or sheep for example autoimmune diseases e.g. rheumans of the breast or liver, ardionascular disorders e.g. cardiac arrest, cerebrovascular disorders cardiovascular disorders e.g. cardiac arrest, cerebrovascular disorders e.g. cardiac arrest, cerebrovascular disorders e.g. Alzheimer's disease, infections caused by bacteria, viruses and fungi and ocular disorders e.g. corneal infection. Many other diseases and
                                                                                                                                                                                                                                                                     Human; ss; gene; secreted protein; gene therapy; immunosuppressive; antiarthritic; antirheumatic; antiproliferative; cytostatic; cardiant; vasotropic; cerebroprotective; motorropic; neuroprotective; antibacterial; virucide; fungicide; opthalmalogical; autoimmune disease; neoplasm; rheumatoid arthritis; hyperproliferative disorder; cardiac arrest; cardiovascular disorder; cerebrovascular disorder; cerebral ischaemia; anglogenesis; nervous system disorder; Alzheimer's disease; infection; coular disorder; corneal infection; wound healing; skin aging; epithelial cell proliferation; food additive.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel 71 isolated secreted polypeptides and polynucleotides encoding the polypeptides, useful for treating Huntington's disease, sepsis, meningitis, thrombocytopaenia, haemolytic anaemia, rheumatoid arthritis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Shi Y;
Soppet DR;
         CCATCCGGCCACGAGACTGCTCCCGGCACGTCCAGAGCAACTTACCCCGGCCAGC 945
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Young PE,
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Florence KA,
                                                                 979
                                                                             CAGCCCTCTCACCCGAGGATCCCTACCCCTGGC
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Komatsoulis G, Duan DR,

The Brower LA, F
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                                                                                                                                                                                                                                              Human secreted protein gene 48
                                                                                                                                                            ABK69773 standard; cDNA; 1050
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Endress GA,
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disorders are listed in the specification. The polypeptides can also be used to aid wound healing an epithelial cell proliferation, to prevent skin aging due to sunburn, to maintain organs before transplantation, for supporting cell culture of primary tissues, to regenerate tissues and in chemotaxis. The polypeptides can also be used as a food additive or preservative to increase or decrease storage capabilities. The present sequence encodes a novel human secreted protein of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer; peripheral nervous system; neuropathy; central nervous system; CNS; Alzheimer's; parkinson's disease; Huntington's disease; heamostatic; amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             525
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                                                                                                                                                                                                                                                                                                    346 GAGGCTGAGGATCAGCAGGCGCGCGCTTCCTGGCGCAGCTGCTGCGCGCGTCTGGGGGCGCCCC 405
                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                               Length 1050;
                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                       Seguence 1050 BP; 172 A; 398 C; 344 G; 136 T; 0 other;
                                                                                                                                                                                                               Score 583; DB 24;
Pred. No. 3.1e-250;
0; Mismatches 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BP.
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99.88;
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                                                                                                                                                                                                                                   Best Local Similarity 99.8
Matches 633; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            22-OCT-2001
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                                                                                                                                                                                                                 Query Match
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Novel 71 isolated secreted polypeptides and polynucleotides encoding the polypeptides, useful for treating Huntington's disease, sepsis, meningitis, thrombocytopaenia, haemolytic anaemia, rheumatoid arthritis,
  293 AGCTGGCGCGGGCGCTGGCCGCATCTGCTGCTGAACGTCAGGAGCGGGGCGGGGCCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Komatsoulis G, Duan DR,
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Mucenski M, Ebner R;
                                                                                                                                                                                                                                                                                                                                                                                                         BP
                                                                                                                                                                                                                                                                                                                                                                                                        ABK69876 standard; DNA; 4503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                                                                                                                                                                                              653 TGTTGAGGTACTTGCTGGG 671
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12-JAN-2001; 2001WO-US00911.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                               638 TGTTGAGGTACTTGCTGGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                            the encoded polypetides (AAMS8642-AAM42131) with noctropic, immunosuppressant and cytostatic activity. The polynucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral nervous system, such as peripheral nervous injuries, peripheral nervous system, such as peripheral nervous system diseases, such as alzaheimer's Parkinson's disease, Huntington's disease, such as alzaheimer's Parkinson's disease, Huntington's disease, such as utilisation of the activities auch as: Immune system suppression, activity, chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, cancer diagnosis and therapy, drug screening, where the contains and inflammation, leukaemias and contains and the contains.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The sequence data for this patent did not form part of the printed
                                                                                                                                                                                                                                                                                       ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            53 GCCCGGCTCGCTGGGGCAGCATGGCGGGTCGCCGCTGCTCTGGGGGCCGCGGGGCCGGGG 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             158 CGCGGCCGGTAAAGGAGCCCCGCGGCCTAAGCGCAGCGTCTCCGCCCTTGGCTGAGACTG 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                           invention relates to human nucleic acids (AAI57798-AAI61369) and
chemokinetic; thrombolytic; drug screening; arthritis; inflammation; leukaemia; ss.
                                                                                                                                                                                                                                                                                       Wang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           38 GCCCGGCTCGCTGGGGGAGCATGGCGGGGTCGCCGCGCTTCTGGGGGGCCGCGGGGCCGGGG 97
                                                                                                                                                                                                                                                                                                                                                                           Novel nucleic acids and polypeptides, useful for treating disorders such as central nervous system injuries -
                                                                                                                                                                                                                                                                                     Ren F, W
Zhang J;
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Yang Y,
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S8.0%; Score 568; DB 22;
Best Local Similarity 99.8%; Pred. No. 1.5e-243;
Matches 618; Conservative 0; Mismatches 1;
                                                                                                                                                                                                                                                                                   Liu C, Asundi V, Chen R, Ma Y,
Wang Z, Wehrman T, Xu C, Xue AJ,
Zhou P, Goodrich R, Drmanac RT;
                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; SEQ ID NO 365; 10078pp; English.
                                                                                                                                                                                          2000US-0653450.
2000US-0662191.
2000US-0693036.
2000US-0727344.
                                                                                                                                        2000US-0488725.
2000US-0552317.
2000US-0598042.
                                                                                                                 26-DEC-2000; 2000WO-US34263
                                                                                                                                                                                2000US-0620312
                                                                                                                                                                                                                                                                                                                                    WPI; 2001-442253/47.
P-PSDB; AAM39006.
                                                                                                                                                                                                                                                          (HYSE-) HYSEQ INC.
                                                               WO200153312-A1
                                                                                                                                                                               19-JUL-2000;
03-AUG-2000;
14-SEP-2000;
                                                                                                                                                     25-APR-2000;
09-JUL-2000;
                                       Homo sapiens
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29-NOV-2000;
                                                                                                                                         21-JAN-2000;
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                                                                                                                                                                                                                                                                                                             Zhao QA,
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Human; ds; secreted protein; gene therapy; immunosuppressive; antiarthritic; antirheumatic; antiproliferative; cytostatic; cardiant; vasotropic; cerebroprotective; notoropic; neuroprotective; antibacterial; virucide; fungicide; opthalmalogical; autoimmune disease; neoplasm; rheumatoid arthritis; hyperproliferative disorder; cardiac arrest; cardiovascular disorder; cerebral ischaemia; angiogenesis; nervous system disorder; Alzheimer's disease; infection; ocular disorder; corneal infection; wound healing; skin aging; epithelial cell proliferation; food additive.
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                                                                                                                                                                                                                                             AGGCGCAGGAGGCTGAGGATCAGCAGGCGCGCGTCCTGGCGCAGCTGCTGCGCGTCTGGG
                                                                                                        GCGCCCCCCCCAACTCTGATCCGGCTCTGGGCTTGGACGACGCCCCGGACGCCCTGCAG
                                                                                                                                                                                                                                                                                                                      518 TTGTCCCCGCCCCGTCCCCGCCGCGCGCTCCCGACCCCCGGCCCCCGGTCTACGACGACG
                                                                                                                                                                                                             CGCAGCTCGCTCGCGCTCTCCGCGCCCCTGACCCTGCCGCCCTAGCAGCCCAGC
                                                                                                                                                                                                                                                                                                                                                                                                                              578 GCCCCGCGGGCCCGGATGCTGAGGAGGCAGGCGACGACGACGTGGACCCCGAGC
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Young PE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human secreted protein gene 49 genomic DNA fragment #2.
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Florence KA,
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Query Match
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                                           fragment, homologue complement or allelic variant) encoding a human secreted protein (and its fragment, domain, epitope, variant, secreted fragment, homologue complement or allelic variant) encoding a human secreted protein (and its fragment, domain, epitope, variant, secreted form and species variant). Also included are a recombinant vector comprising the nucleic acid and are recombinant host cell that expresses the secreted protein and a method of identifying a binding partner of the secreted protein and a method of identifying a binding partner of the secreted protein and method of identifying a binding compared of the secreted protein and method of identifying a binding partner of the secreted protein and method of identifying a binding commands, mice, rabbits, goats, horses, cats, dogs, chickens or sheep of creample autoimmune diseases e.g. rheumatoid arthritis, hyperpooliferative disorders e.g. cardiac arrest, cerebrovascular disorders e.g. cardiac arrest, cerebrovascular disorders e.g. cardiac arrest, cerebrovascular disorders e.g. corneal infections system disorders e.g. corneal infections many other diseases and cused to aid wound healing an epithelial cell proliferation, to prevent skin aging due to sunburn, to maintain organs before transplantation, for supporting cell culture of primary tissues, to regenerate tissues and in chemorate and properting cell cultures of primary tissues, to regenerate tissues and in chemorate represent as expensed as a food additive or chemotrasts. The polypeptides can also be used as a food additive or sequence represents a ds DNA fragment of the gene for a novel human certified to anyeling or an envel human certified to anyeling cell and anyeling cell or anyeling cell and anyeling cell anyeling cell
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          170 AGGAGCCCCGCGCGCCTAAGCGCAGCGTCTCCGCCCTTGGCTGAGACTGGCGCTCCTCGCC 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CGCTGGCGCATCTGCTGGAGGCCGAACGTCAGGAGCGGGCGCGGGGGCGAGGCGAGGAGG 349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CTGAGGATCAGCAGGCGCGCGTCCTGGCGCAGCTGCTGCGGCGCGTCTGGGGCGCCCCCCCGCA 409
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     646
                                 invention relates to an isolated nucleic acid molecule (or its
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 4503;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 4503 BP; 783 A; 1181 C; 1314 G; 1225 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 375; DB 24;
Pred. No. 1.5e-157;
0; Mismatches 2;
Example 2; Page 1404-1406; 1478pp; English.
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ABN95203/c
ID ABN95203 standard; DNA; 301 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          38.3%;
99.6%;
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The invention relates to a novel method for diagnosing and detecting the progression of liver cancer, hepatocellular carcinoma or metastatic liver tumour in a patient, and differentiating metastatic liver cancer from hepatocellular carcinoma in a patient, involving detecting the level of expression of two or more genes represented in ABN93503-ABN97455 in a tissue sample. The method of the invention has hepatocropic, and cytostatic activity. The method is useful for diagnosing and detecting the progression of liver cancer, hepatocellular carcinoma and metastatic liver carcinoma in a patient. The method is useful for identifying expression profiles which serve as useful diagnostic markers as well as markers that can be used to monitor disease states, disease progression, drug efficacy and drug metabolism.

Note: The sequence data for this patent did not form part of the printed as procession, the content of the printed as the cast of the printed as the c
                                                                                             Gene; liver cancer; ds; hepatocellular carcinoma; hepatotropic; metastatic liver tumour; cytostatic; expression profile; disease state; disease progression; drug toxicity; drug efficacy; drug metabolism.
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Gene #1701 used to diagnose liver cancer.
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(first entry)

13-AUG-2002 ABN95203;

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The present invention describes a method (M1) for screening for an anti-neoplastic agent. The method involves exposing cells to a chemical agent to be tested for anti-neoplastic activity, determining a change in expression of at least one gene (I) of a signature gene set, where (I) comprises a sequence (S) selected from 8447 sequences (given in ABL61664 to ABL70110), or is at least 95% identical to (S), where a change in extivity and can be used in gene therapy. MI can be used for screening an anti-neoplastic activity, (I) has cytostatic activity and can be used in gene therapy. MI can be used for screening an anti-neoplastic agent, and can be used for producing a product which is the data collected with respect to the anti-neoplastic agent as a result of MI, and the data is sufficient to convey the chemical structure and/or properties of the agent. MI can be used in the treatment of cancer such as colon, breast, stomach, lung, thyroid, coscophageal, ovarian, kidney, prostate or pancreatic cancer, adenocarcinoma, carcinoma, clear cell cancer, infiltrating ductal cancer, infiltrating ductal cancer, infiltrating ductal cancer, infiltrating ductal cancer.
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Screening for anti-neoplastic agent involves exposing cells to a chemical agent to be tested for anti-neoplastic activity, and determining a change in expression of a gene of a signature gene set
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 23.1%; Score 226; DB 24; Length 301; Best Local Similarity 99.6%; Pred. No. 5e-91; Matches 276; Conservative 0; Mismatches 1; Indels
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stomach; lung; prostate; pancreas; carcinoma; antitumour; cancerous;
cytostatic; gene therapy; antineoplastic; Wilm's tumour; adenocarcinoma;
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                                                                                                                                                                                                                     Kidney cancer related gene sequence SEQ ID NO:6724.
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22-SEP-2000;
22-SEP-2000;
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02-MAY-2001; 2001US-287724P.
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(COMP-) COMPUGEN INC.

Mintz L, Faigler S; Mintz E, Wasserman A, Shoshan A,

New oligonucleotide libraries comprising oligonucleotides which selectively hybridize to mRNAs transcribed from a transcription unit of a genome, useful for detecting tissue-', pathology-', and WPI; 2002-257383/30.

Example 1; SEQ ID 14889; 47pp; English.

developmental-specific genes

transcription units that populate a genome. The library comprises several oligonuclectides, each capable of hybridising selectively to a several oligonuclectides, each capable of hybridising selectively to a set of messenger RNA transcribed from a given transcription unit of the genome, which encodes one or more messenger RNA splice variants. The oligonuclectide libraries are useful for detecting mRNAs from a biological sample, in expression profiling studies, in qualitatively or quantitatively characterising the corresponding transcriptome, and in detecting RNA transcripts and splice variants of human or animal currently of transcripts and splice variants of human or animal confitcular biological transcripts of a sub-transcriptome under a particular biological or pathological state, and so allowing the detection of tissue and pathology-specific genes such as those genes only expressed in specific tissue under a specific pathological condition; to detect developmental specific genes; and to detect RNA transcripts and splice variants of a transcriptome of a patient suffering from a particular disorder. ABN27253 to ABN59589 represent The present invention describes oligonucleotide libraries for detecting messenger RNAs that populate a (sub-)transcriptome, where the (sub-)transcriptome comprises messenger RNAs transcribed from multiple the exemplification of the present invention.

N.B. The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wlpo.int/pub/published\_pct\_sequences.

Sequence 60 BP; 12 A; 16 C; 21 G; 11 T; 0 other;

ö / Match 6.1%; Score 60; DB 24; Length 60; Local Similarity 100.0%; Pred. No. 5.8e-17; les 60; Conservative 0; Mismâtches 0; Indels Query Match Best Loca Matches

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606 AGGCGACGACGACGTGGACCCCGAGCTGTTGAGGTACTTGCTGGGACGGATTCT 665 1 AGGGACGAGACACCCGACGTGGACCTGATTGATGAGGTACTTGCTGGGACGGATTCT 60 ŏ

Search completed: April 12, 2003, 19:33:48 Job time : 286 secs

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1 MAGSPLLWGPRAGGVGLLVLLLLGLFRPPPALCARPVKEPRGLSAASPPLAETGAPRRFF 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
PROSAAS precursor (Granin-like neuroendocrine peptide precursor).
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE-CTERUS;
Strausberg R.;
Submitted (EB-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AF181562; AAF22643.1; -.
EMBL; BC002851; AAH02851.1; -.
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27372 MW; FF8E2722784B7A5C CRC64;
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J. Neurosci. 20:0-0(2000).
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                                                                        April 4, 2003, 14:14:10 ; Search time 87 Seconds (without alignments) 615.773 Million cell updates/sec
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                                                                                                                                                         1 MAGSPLLWGPRAGGVGLLVL......RVKRLETPAPQVPARRLLPP 260
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GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
                                                     OM protein - protein search, using sw model
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Q9RSN4
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sp_bacteriap:*
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sp_phage:*
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sp_bacteria:*
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Length 260; Indels

Score 1319; DB 4; Pred. No. 3.8e-74;

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Q9GZF7 Q9L0J8 Q96G51 Q9L1H8 Q93HH0	034003 Q23635 Q9S2Q5 Q9AD96 Q9Z1P7 Q96SB3	Q9VGC1 Q69270 Q9K452 Q9RJYS Q9GRZ3 Q9GJL0 Q9JJL0	Q8VHK2 Q99JK6 Q9UDW8 Q9ZIW5 Q8VPM8 Q9ZIR1	070373 09AG79 093HJ5 09H0J3
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                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus. NCBL_TaxID=10116;
                PALGLODDPDAPAAQLARALLRARLDPAALAAQLVPAPVPAAALRPRPPVYDDGPAGPDA 180
                                                                             EEAGDETPDVDPELLRYLLGRILAGSADSEGVAAPRRLRRAADHDVGSELPPEGVLGALL 240
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                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. MEDLINE-20098938; PubMed-10632593; Fricker L., McKinzie A.A., Sun J., Curran E., Qian Y., Yan L., Patterson S.D., Courchesne P.L., Richards B., Levin N., Mzhavia N.,
      RSVPRGEAAGAVQELARALAHLLEAERQERARAEAQEAEDQQARVLAQLLRVWGAPRNSD
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                                                                                                                                                                                                                                                                                                                                                                                                    DB 11; Length 260;
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C84F688BDEB5313E CRC64;
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                     32;
                                                                                                                                                                                                                                                                                                                                                                                                   Score 1102; DB 1:
Pred. No. 8.6e-61
8; Mismatches 3:
                                                                                                                                                                             260 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               258 AA.
                                                                                                                                                                                              Created)
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                                                                                                                                                                                                                                                                                                                                      processing.";
J. Neurosci. 20:639-648(2000).
EMBL; AF181561; AAF22642.1; -.
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SEQUENCE 260 AA; 27414 MW;
                                                                                                              RVKRLETPAPQVPARRLLPP 260
                                                                                                                                                                                                                                                                                                                                                                                                   83.5%;
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RVKRLENSSPQAPARRLLPP 260
                                                                                                                                                                                            01-MAY-2000 (TrEMBLrel. 13, 01-MAY-2000 (TrEMBLrel. 13, 01-DEC-2001 (TrEMBLrel. 19,
                                                                                                                         Best Local Similarity 84.6
Matches 220; Conservative
                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                Rattus norvegicus (Rat).
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                                                                                                                                                                                                                      ProSAAS precursor.
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Best Local S
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ID Q91W26
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61 RSVPRGEAAGAVQELARALAHLLEAERQERARAEAQEAEDQQARVLAQLLRVWGAPRNSD 120
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01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Similar to granin-like neuroendocrine peptide.
Mus musculus (Mouse)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostoml;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus.
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Mus musculus (Mouse).

Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;

Mammalia, Eutheria, Rodentia, Sciurognathi; Muridae; Murinae; Musinae; Musin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 258;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
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Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC012263; AAH12263.1; -.
SEQUENCE 258 AA; 27270 MW; 4197C8B077A20A22 CRC64;
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07452A460E868CF6 CRC64;
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Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            82.0%; Score 1082; DB 11
83.5%; Pred. No. 1.5e-59;
ive 10; Mismatches 31
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EMBL; AF181560; AAF22641.1; -.
MGD; MGI.135431; POSKIN.
InterPro; IPR002965; P_rich_extensn.
PRINTS; PR01217; PRICHEXTENSN.
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27285 MW;
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01-MAY-2000 (TrEMBLrel. 13,
01-MAY-2000 (TrEMBLrel. 13,
01-UNN-2002 (TrEMBLrel. 21,
ProSAAS precursor.
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                                                                                                                                        1 MAGSPLLWGPRAGGVGLLVLLLLGLFRPPPALCARPVKEPRGLSAASPPLAETGAPRRFR
                                                                                                                                                                                                                           RSVPRGEAAGAVQELARALAHLLEAERQERARAEAQEAEDQQARVLAQLLRVWGAPRNSD
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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  Length 258;
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                                                           Indels
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Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AF293356; AAGG9048.1;
SEQUENCE 187 AA; 19940 MW; 041F1F858591A9B0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Last sequence update)
Last annotation update)
Score 1076; DB 11;
Pred. No. 3.4e-59;
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60.6%; Pred. No. 2.7e-23;
tive 5; Mismatches 40;
                                                     10; Mismatches
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MEDLINE-98292390; PubMed=9630436;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RVKRLETPAPQVPARRLLPP 260
81.6%;
83.1%;
                                                           Conservative
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Matches 117; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
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                          Similarity
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Q9ESU4;
01-MAR-2001 (
Query Match
Best Local (
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RESULT

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MEDLINE-21608551; PubMed-11743194;
Goodner B., Hinkle G., Gattung S., Miller N., Blanchard M.,
Ourchlo B., Goldman B.S., Cao Y., Askenazi M., Halling C., Mullin L.,
Houmiel K., Gordon J., Vaudin M., Iartchouk O., Epp A., Liu F.,
Wollam C., Allinger M., Doughty D., Scott C., Lappas C., Markelz B.,
Flanagan C., Crowell C., Gurson J., Lomo C., Sear C., Strub G.,
Clelo C., Slater S.,
"Genome sequence of the plant pathogen and biotechnology agent
Agrobacterium tumefaciens C58.",
Science 294:2232-2288(2001).
EMBL; AE008982; AAL4112.1; -.
EMBL; AE008982; AAL4112.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-21608550; PubMed-11743193; Wood D.W., Setubal J.C., Kaul R., Monks D.E., Kitajima J.P., Wood D.W., Setubal J.C., Kaul R., Mond G.E., Almelda N.F. Jr., Woo L., Chen Y., Zhou Y., Chen L., Wood G.E., Almelda N.F. Jr., Woo L., Chen Y., Paulsen I.T., Eisen J.A., Karp P.D., Bovee D. Sr., Chapman P., Clendenning J., Deatherage G., Gillet W., Grant C., Kutyavin T., Levy R., Li M.-J., McClelland E., Palmieri A., Kutyavin T., Levy R., Li M.-J., McClelland E., Palmieri A., Rouse G., Saenphimmachak C., Wu Z., Romero P., Gordon D., Zhang S., Yoo H., Tao Y., Biddle P., Jung M., Krespan W., Perry M., Gordon-Kamm B., Liao L., Kim S., Hendrick C., Zhao Z.-Y., Dolan M., Chumley F., Tingey S.V., Tomb J.-F., Gordon M.P., Olson M.V.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           : || |:|| | ::|| || ::|| || EARRRA---KMEAANRAAEEAAAK 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DDPDAPAAQLARALLRARLDPAALAAQLVPAPVPAAALRPRPPVYDDGPAGPDAEEAGDE 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       187 TPDVDPELLRYLLGRILAGSADSEGVAAPRRLRRAADHD-----VGSELPPEGVLGAL 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "The genome of the natural genetic engineer Agrobacterium tumefaciens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  187 VAASQPAAEV-----RAEPASERPAAAAAPAPRTDARPQ-----SAAAAPRSAPA---
                                                            01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
11-JUN-2002 (TrEMBLrel. 21, Last annotation update)
12-JUN-2002 (TrEMBLrel. 21, Last annotation update)
13-JUN-2002 (TrEMBLrel. 21, Last annotation update)
13-JUN-2003 (ARC. 2131.
13-JUN-2003 (Strain C58 / ATCC 33970).
13-JUN-2004 (Strain 21) (Strain C58 / ATCC 33970).
13-JUN-2004 (Strain 21) (Strain C58 / ATCC 33970).
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913 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Initiation factor; Complete proteome. SEQUENCE 913 AA; 98821 MW; 2BF1CI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Science 294:2317-2323(2001).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 25.29
Matches 65; Conservative
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                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=176299;
                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nester E.W.;
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ID 09
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he human GNAS1 gene is imprinted, and encodes a paternally expressed protein XL alpha s, in addition to the biallelically expressed Gs
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                                                                                                                                                                                                                                                                                                                                                                                              107 AQLLRV----WGAP------RNSDPALG-LDDDPDAPAAQLARALLRARL 145
                                                                                                                                                                                                                                                                                                                                                                                                                              67 AEGGKVPSPGYGSPAAGAASADTAARAAPADPDSGATPEDPDSGTAP-----ADP 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                               146 DPAALAAQLVPAPVPAAALRPRPPVYDDGPAGPDAEEAGDETPDVDPELLRYLLGRILAG 205
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           168 AA-PEAPAAPAAAETRAAHVAPAAPDAGAPTAPAASATRAAOVRRAASAAPASGARRKIH 226
                                                                                                                                                                                                                                                                                                                                                              26 SPPIALDGPPIK-----VSGAPD-----KRERAERPPVEEEAAEMEGAADA 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDITRE-20036896; PubMed=10567266; White O., Eisen J.A., Heidelberg J.F., Hickey E.K., Peterson J.D., Dodson R.J., Haft D.H., Gwinn M.L., Nelson W.C., Richardson D.L., Moffat K.S., Qin H., Jiang L., Pamphile W., Crosby M., Shen M., Vamathevan J.J., Lam P., McDonald L., Utterback T., Zalewski C., Makarova K.S., Aravind L., Daly M.J., Minton K.W., Fleischmann R.D. Ketchum K.A., Nelson K.E., Salzberg S., Smith H.O., Venter J.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DSGAFAADPDSGAAPAAPADPDSGAAPDAPADPDSGAAPDAPADPD------AG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Deinococcus radiodurans.
Bacteria; Thermus/Deinococcus group; Deinococci; Deinococcales;
Deinococcaceae; Deinococcus.
                                                                                                                                                                                                                                                                  DB 4; Length 441;
                                                    submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.

DR EMBL; AJ224868; CAA12165.1; --
DR EMBL; AJ224868; CAA12165.1; --
DR InterPro; IPR001019; Gprotein_alpha.

R Pfam; PF00503; Galpha; 1.

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SEQUENCE 441
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                                                                                                                                                                                                                                                                                                  Indels
                                                 alpha.";
Submitted (JUL-1998) to the EMBL/GenBank/DDBJ databases
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553 AA; 59078 MW; 18DD1B4AE4195A8B CRC64;
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Last annotation update)
                                                                                                                                                                                                                                                               10.3%; Score 136.5; DB 4; 27.5%; Pred. No. 0.4; tive 19; Mismatches 89;
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Science 286:1571-1577(1999).
EMBL; AE002044; AAF11639.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-MAY-2000 (TIEMBLEEL 13, 01-MAR-2002 (TIEMBLEEL 20, Hypothetical protein DR2090.
                                                                                                                                                                                                                                                                                                  Conservative
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                                                                                                                                                                                                                                                                                 Local Similarity
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                                                                                                                                                                                                                                                                                                 67;
                                                                                                                                                                                                                                                                Query Match
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Q9RSN4
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                           01-OCT-2000 (TTEMBLEL 15, Last sequence update)
01-JUN-2001 (TTEMBLEL 17, Last annotation update)
XLalphas protein (DJ806M20.3.1) (Isoform 1 of guanine nucleotide
binding protein (G protein), alpha stimulating activity polypeptide 1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        47 SPPLAETGAPRRFRRSVPRGEAAGAVQELARALAHLLEAERQERARAEAQEAEDQQARVL 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       107 AQLLRV----WGAP------RNSDPALG-LDDDPDAPAAQLARALLRARE 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DPAALAAQLVPAPVPAAALRPRPVYDDGPAGPDAEEAGDETPDVDPELLRYLLGRILAG 205
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AA-PEAPAAPAABETRAAHVAPAAPDAGAPTAPAASATRAAQVRRAASAAPASGARRKIH 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   120 DSGAFAADPDSGAAPAAPADPDSGAAPDAPADPDSGAAPDAPADPD------AG
                                                                                                                            Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           69;
                                                                                                                                                                                                                           MEDLINE-20215313; Pubmed-1074992;
Hayward B.E., Bonthron D.T.;
"An imprinted antisense transcript at the human GNAS1 locus.";
Hum. Mol. Genet. 9:835-841(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 388;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                        Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ251760; CAB83215.1; -.
EMBL; AL132655; CAC07997.1; -.
InterPro; IPR00119; Gprotein_alpha.
Pfam; PF00503; G-alpha; 1.
NON_TER 388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bonthron D.T.;
Submitted (MAR-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE 388 AA; 39996 MW; 51A91A227C3AAEA4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         89;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ch 10.3%; Score 136.5; DE Similarity 27.5%; Pred. No. 0.35; 67; Conservative 19; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-NOV-1998 (TrEMBLrel. 08, Created)
01-NOV-1998 (TrEMBLrel. 08, Last sequenc
01-JUN-2001 (TrEMBLrel. 17, Last annotat
GNAS1 protein (DJ806M20.3.2) (Fragment).
                                                                                                (Fragment).
XLALPHAS OR GNAS1.
                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      [1]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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SEQUENCE FROM N.A.
                                                                                                                                                                               NCBI_TaxID=9606;
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LRPP 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
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PTAEAASGGGSAEGTDVVLPALGESVTEGTVTRWLKSV--GDSVEADEPLLEVSTDKVDT 178
                                                                                               86 ERQERARAEAQE---AEDQQARVLAQLLRVWGAPRNSDPALGLDDDPDAPAAQLARALLR 142
                                                                                                                            236 ААРАРААРАРАРДАРАРДАРБАРДООТАРАРДРАРАРАРАРАРАРАРАРАРАРАРАР
                                                                                                                                                                                                                                                                                  DAEEAGDETPDVDPELLRYLLGRILAGSADSEGVAAPRRLRRAADHDVGSELPPEGVLGA 238
                                                                                                                                                                                                                                                                                                                           296 TATOATDEGAYVTP-LVRKLAAESSVDLASVKGTGVGGRIRK-------QDVIAA 342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Du H., Minx P., de la Bastide M., Nascimento L., Spiegel L., Preston R., Kirchoff K., Kuit K., Baker J., Vil M.D., Zutavern T., Santos L., Cunnius D.M., Rodriquez S., Miller B., Balija V., Shah R., Babret A., King L., O'Shaughnessy A., Palmer L., Dedhia N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              137 LATLLPRLIRCPHRACPASPPPPRLIRPATLASPP-PRLLRPRRARISVAPRSRAAPAAA 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ELARALAHILEAERQERARAEAQEAEDQQARVLAQLIRVWGAPRNSDPALGLDDDPDAPA 133
       PPALCARPVKEPRGLSAASPPLAET --- GAPRRFRRSVPRGEAAGAVQELARALAHLLEA 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18 LVLLLLGLFRPPPALCARPVKEPRGL --- SAASPPLAETGAPRRFRRSV - PRGEAAGAVQ 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Oryza sativa (Rice), and Stroptophyta; Embryophyta; Tracheophyta; Spermatophyta; Enthartoideae; Oryzae, Or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Genomic sequence for Oryza sativa, Nipponbare strain, clone OSJNBa0095C06, from Chromosome 10, complete sequence."; Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 492;
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11.4%; Pred. No. 0.98;
.ve 11; Mismatches 108; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hypothetical protein.
SEQUENCE 492 AA; 52539 MW; 23ABC4531C2587E6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Hypothetical 52.5 kDa protein.
0SJNBA0095C06.3 OR OSJNBA0091J06.20.
                                                                                                                                                                                       143 ARLDPAALAAQLVPAPVPAAALRPRP-----PVYDDGPA----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        492 AA
                                                                                                                                                                                                                                                                                                                                                                        239 LLRVKRLETPAP---QVPA 254
                                                                                                                                                                                                                                                                                                                                                                                                                      343 AEAAKAAAAPAAAAAAA 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   31.4%;
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Best Local Similarity 31.4%,
Matches 81; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=NIPPONBARE;
Du H., Minx P., de
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28RV89;
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       53
                                                  121
                                                                                                                                          179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-99078078; PubMed-9858775; Youn H.D., Kah Y.C., Kang S.O.; Youn H.D., Hah Y.C., Kang S.O.; Ilipoamide dehydrogenase from streptomyces seoulensis: biochemical and genetic properties.";
                                                                                                                                                                                                                                                                                                                                                                                              205 KPAPA--PQP---DSDPSLPRTLQEALASDRLPDLPVELLERLWEQEQEAQAQEQEEPAPAP 259
                                                                                                                                                                                                                                                                                                            159 VPAAALRPRPPVYDDGPAGPDAEE---AGDETPDVDPELLRYLLGRILAGSADSEGVAAP 215
                                                  Gaps
                                                                                                                                                                                   54 GAPRRFRRSVPRGEAAGAVQELARALAHLLEAERQERAR------AEAQEAEDQQAR 104
                                                                                                                                                                                                                                92 VAPTRISRSARARPIPAETVPSAPVQAPVAEARPEPKPRPPIKAAAPVPAASPAEETEAA 151
                                                                                                                                                                                                                                                                           105 VLAQLIRVWGAPRNSDPALGLDD---DPDAPAAQLARALLRARLDPAALAAQ---LVPAP 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                             ----- LAET 53
                                                                                                                                        32 GTLAPEAPVQIRPVRRPAGQVPTTSIEALSGVEPPAPRAEVQVRAYRDPSRRTPTAAEEP 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
NCBI_TaxID=73044;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    51;
DB 2; Length 612;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10.0%; Score 132.5; DB 2; Length 27.0%; Pred. No. 0.99; Live 21; Mismatches 117; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.

Youn H., Kang S.-O.;
Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases.
-1- SIMILARITY:
-CONTAINS 2 LIPOYL-BINDING DOMAINS.
EMBL: AF047034; AAD17484.2;
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HSSP; P11961; 2PDD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       612 AA; 61368 MW; B804109089943056 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ProDom; PD001115; 20xoacid_dh; 1.
PROSITE; PS00189; LIPOYL; 2.
PROSITE; PS00430; TONB_DEPENDENT_REC_1; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              216 RRLRRAADHDVGSELPPEGVLGALLRVKRLETPAPQVPAR 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GLFRPPPALCARPVKEPRG-----LSAASPP-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              612 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Biochim. Blophys. Acta 1388:405-418(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR001078; 20xoacid_dh.
InterPro; IPR000089; Biotin_lipoyl.
InterPro; IPR004016; Bi_binding.
InterPro; IPR003016; Lipoyl.
InterPro; IPR003265; P_rich_extensn.
InterPro; IPR00531; TonB_boxC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Dihydrolipoamide acetyltransferase.
PDHB.
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Pfam; PF00164; biotin_lipoyl; 2.
Pfam; PF02817; e3_binding; 1.
PRINTS; PR01217; PRICHEXTENSN.
PRINTS; PR01574; TUBBYPROTEIN.
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                                               Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Streptomyces seculensis.
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Matches 70; Conserv
                       Similarity
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         Local Sim.
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  Query Match
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                          Best Loc
Matches
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13;

Gaps

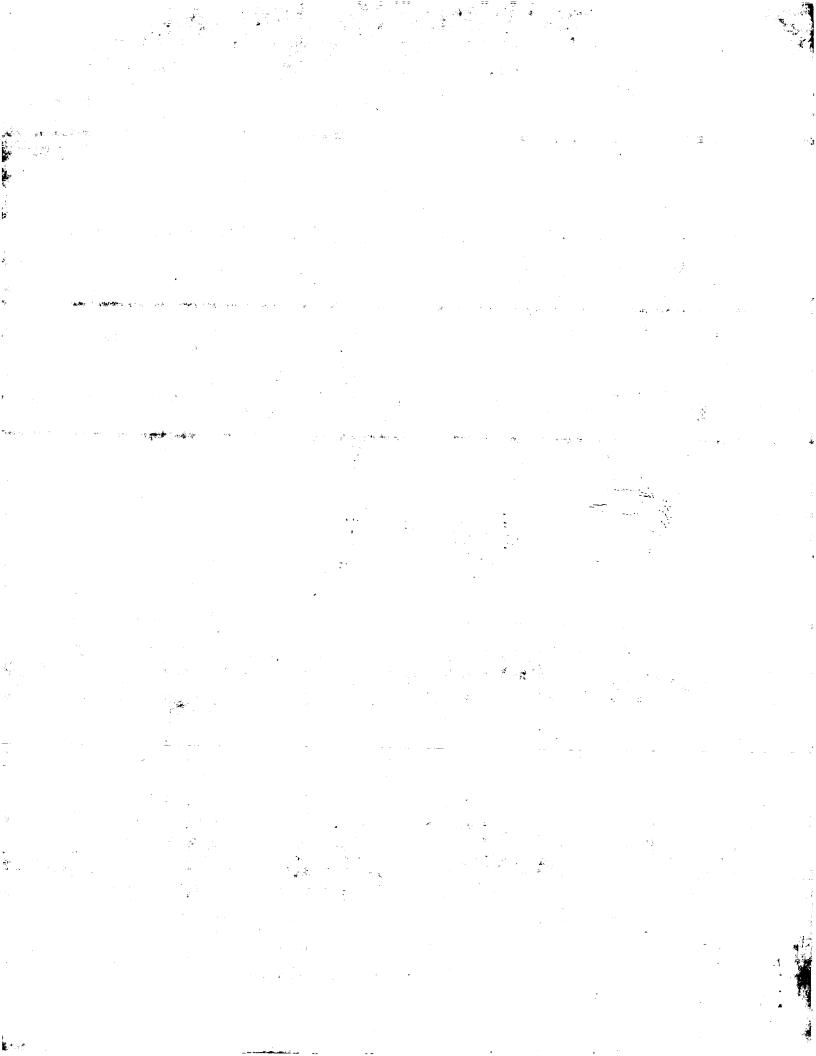
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Best_Local Similarity 29.8
Matches 82; Conservative
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                                                                                                                                                                                         NCBI_TaxID=155892;
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                    AQLARALLRARLDPAALAAQLVPAPVPAAALRPRPPVYDDGPAGPDAEEAGDETPDVDPE 193
                                                                                                                                                               284 LLRSTCAALPHRRRLASSTPASRLAATLATLLPRLLRCPHRACPASPPPR-----LLRP 338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RR--SVPRGEAAGAVQ-ELARALAHLLEAERQERARAEAQEAEDQQARVLAQLLRVWGAP 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       117 RNSDPALGLDDDPDAPAAQLARALLRARLDPAALAAQLVPAPVPAAALRPRPPVYDDGPA 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     177 GPDAEEAGDETPDVDPELLRYLLGRILAGSADSEGVAAPRRLRRAADHDVGSELPPEGVL 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Leishmania major.
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.
NCBI_TaxID=5664;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ----RRF 59
                                                               -----RILR----PATLASP-----PPRLLRPRRARLSVAPRSRAAPAAA-----R
                                                                                                                  194 LLRYLLG-----RILAGSADSEGVAA-----PRRLRRAADHDVGSELPPEGVLGALLRV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       208 GGSLPK---TEDTEATAHRQAAASARVAPMPASRRSDSSATPSASTAISPPPPA---SPT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           72;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ivens A.C., Lewis S.M., Bagherzadeh A., Zhang L., Chan H.M., Smith D.F.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           th 9.9%; Score 131; DB 5; Length 1290; Similarity 26.6%; Pred. No. 2.6; 69; Conservative 23; Mismatches 95; Indels 7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "A physical map of the Leishmania major Friedlin genome.";
Genome Res. 8:135-145(1998).
Bmbi, ALIG1414; CAB77679.1; -.
Hypothetical protein.
SEQUENCE 1290 AA: 136159 MW; 6A6F8BB395CE6818 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Masuy D., Purnelle B., Goffeau A., Ivens A.C., Quail M., Rajandream M.A., Barrell B.G.; Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                            01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Hypothetical 136.2 kDa protein.
                                                                                                                                                                                                                                                                                                                                                                                       PRT; 1290 AA.
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                                                                                                                                                                                                                243 KRLETPAPQVPARRLLPP 260
                                                                                                                                                                                                                                                                339 ATLASPPP----RLLRP 351
                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
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ID Q9A718
AC Q9A718;
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MEDINE-2113698; PubMed-11259647;
Mierman W.C., Feldblyum T.V., Laub M.T., Paulsen I.T., Nelson K.E.,
Bisen J., Heidelberg J.F., Alley M.R.K., Ohta M., Maddock J.R.,
Potocka I., Nelson W.C., Newton A., Stephens C., Phadke N.D., Ely B.,
DeBoy R.T., Dodson R.J., Durkin A.S., Gwinn M.L., Haft D.H.,
Kolonay J.F., Smit J., Craven M.B., Khouri H., Shetry J., Berry K.,
Utterback T., Tran K., Wolf A., Vamathevan J., Ermolaeva M., White O.,
Salzberg S.L., Venter J.C., Shapiro L., Fraser C.M.;
Compleace genome sequence of Caulobacter crescentus.";
Proc. Natl. Acad. Sci. U.S. A. 98:4136-4141(2001).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         336 PPQKTAERSPGKVALGGASLPALVQLEPRDGEGEPPATEPAEPRPLMTRGYGAPVEDVRS 395
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STRAIN-ATCC33701; PLASMID-PREAT701 (P33701);
Takai S., Sekizaki T., Kakuda T., Nakamura M., Suzuki K., Ogino N.;
Takai G.EB-2000) to the EMBL/GenBank/DDBJ databases.
[2]
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                182 AAAPPSAVGAAP----PMVAEGDLKAALWVLRSALSAWLAKAEVSSGAVAPHVGSVADDG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           144 RLDPAALAAQLVPAPVPAAALRPRPPVYDDGPAGPDAEEAGDETPDVDPEL-LRY----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -----LLGRILAGSA------DSEG-----VAAPRRLRR----AADHDVGS
                                                                                                                                    Caulobacter crescentus.
Bacteria; Proteobacteria; alpha subdivision; Caulobacter group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           87;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 16; Length 589;
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Bacteria; Firmicutes; Actinobacteria; Actinobacteridae; Actinomycetales; Corynebacterineae; Nocardiaceae; Rhodococcus.NCBI_TaxID=43767;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hypothetical protein; Complete proteome.
SEQUENCE 589 AA; 59269 MW; A7E52050C891B98A CRC64;
(TrEMBLrel. 17, Created)
(TrEMBLrel. 17, Last sequence update)
(TrEMBLrel. 21, Last annotation update)
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1-WAR-2001 (TrEMBLrel. 16, Last sequence update)
01-WAR-2001 (TrEMBLrel. 16, Last annotation update)
Hypothetical 37.5 kDa protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        91;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  396 KTPPPPYAGGPTAGORPEPTPSLSWAPEAMARRLL 430
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9.9%; Score 130.5; 29.8%; Pred. No. 1.3
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                                                                              Hypothetical protein CC1908
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STRAIN-ATCC 19089 / CB15;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                147 P----AALAAQL--VPAPVPAAAL--RPRPPVYDDGPAGPDAEE--AGDETPDVDPELLR 196
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                                                                                                                                                                                                                                                                                                                                                                          65 R----GEAAGA-----VQELARAL-----AHLLEAERQERARAEAQEAED--- 100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                62 SVPRGE-----AAGAVQELARALAHLLEAERQERARAEAQEAEDQQARVLAQ---LLR 111
                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                             Gaps
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                   STRAIN-ATCC33701, AND 103; PLASMID-PREAT701 (P33701), AND VIRULENCE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                          90;
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                                                                                                                                                                                                                                          Length 350;
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                                                                                                                                                                                                                                                                          89; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Strauberg R.;
Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC019977; AAH19977.1; -..
Hypothetical protein.
SEQUENCE 544 AA; 59840 MW; 075828F5B370111A CRC64;
                                                                                                                                                                                                        56A73F73318B62C3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
1-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Hypothetical 59.8 kba protein.
Mus musculus (Mouse).
                                                                                                                                                                                                                                      Query Match 9.9%; Score 130; DB 2; Best Local Similarity 28.4%; Pred. No. 0.8; Matches 79; Conservative 20; Mismatches 89
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                                                                                                                                  Infect. Immun. 68:6840-6847(2000).
EMBL; AP001204; BAB15640.1; -.
BMBL; AF116907; AAG21734.1; -.
Hypothetical protein: Plasmid.
SEQUENCE 350 AA; 37537 WW; 56A
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Best Local Similarity 25.9%
Matches 74; Conservative
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TISSUE-SALIVARY GLAND;
SEQUENCE FROM N.A.
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Maximum Match 100%
Listing first 45 summaries
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em_htgo_mus:*
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em_htg_rod:*
em_htg_mam:*
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Maximum DB seq length: 2000000000
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Perfect score:
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Pred. No. is the number of results predicted by chance to have a

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score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result		& Query						
		Score	Match	Length	80	ID	 	Description	ption
	10		98.0	966	90	AX083428		AX08342	Sequence
		940		696		AF181562		AF181562	Homo
		776.8		780	9	118		AX0834]	
		υ υ υ υ		1027		AF181560		AF18156	
		580.2		975		BC012263		BC0123	1 12
		502.2		1025	7	AF293356		AF293	enw 9
		174.2		113853		AF196971		AF19697	Ношо
		343		62396		AC098339		AC09833	Rattus
		343		111948		AC094563		AC0984	3 Rattus no
	13	332.6		151694		AL670169		AL6701	9 Mouse
		9.808		177613		AC123014		AC12301	Rattus
	15	276.6		301		AX336215		AX33621	
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		122.4		177613		AC123014		AC1984	/3 Kattus no
	13	66		210215		AC097157		AC0971	Rattus
	20	98.2		206773		AC126296		AC126296	Rattus
	21	93.2		74721		AC096161		AC09616	Rattus
	22	92.2		991		PM12H12B		AL6844	Peni
	533	92		136551		AC048354		AC0483	Homo sa
	4 C	91.4 01		184410		AC128138		AC1281	Kattus
	26	9.06		74721		AC096161		AC09616	1 Rattus no
	27	90.2		110958		AC118521		AC11852	Rattus
		90		1393		PM11H12G		AL6842	264 Penicilli
	53	89.8		151730		AC125640		AC12564	Rattus
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	 מדאוניסאוס		Eukaryota; M	Eukaryota; Metazoa			Š	٠.	Euteleostomi;
	 REFERENCE		malia; (bases	Eutheria; 1 to 998)	. (8 (8)	Primates; Catarrhini	hini; Hom	::	Ното.
_	AUTHORS		Kato, S. ar	d Kimur	T, T	, S. and Kimura, T.	1		
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Patent: WO 0112660-A 120 22-FEB-2001;
SAGAMI CHEMICAL RESEARCH CENTER (JP) ; Protegene
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Pred. No. 2.9e-104;
5; Mismatches 2;
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/note="unnamed protein product"
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Web site:

"Intp://www.nisc.nih.gov/
Contact:
Shevchanko, X., Wetherby, K.D., Beckstrom-Sternberg, S.M.,
Benjamin, B., Blakesley, R.W., Bouffard, G.G., Brinkley, C., Brooks, S.,
Dietrich, N.L., Gunn, X., Gupta, J., Ho, S.-L., Karlins, E., Legaspi, R.,
Lim, M., Maduro, O.L., Masiello, C., Mastrian, S.D., McCloskey, J.C.,
McDowell, J., Pearson, R., Snyder, B., Stantripop, S., Thomas, P.J.,
Zhang, L.-H. and Green, E.D.
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Primates, Catarrhini, Hominidae, Homo.
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Submitted (05-F8B-2001) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Clone distribution: MGC clone distribution information can be fou through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAL Plate: 12 Row: n Column: 24 the series of This clone was selected for full length sequencing because it passed the following selection criteria: GenomeScan gene
GGGCTCTGAGCTGCCCCCTGAGGGCGTGCTGGGGGGCGCTGCTGCGTGTGAAACGCCTAGA 786
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                                                                                 915 AGCACGTCCAGAGCAACTTACCCCGGCCAGCCAGCCTCTCACCCGAGGATCCCTACCC
                                                      GACCCCGCCCCCCCCCCCCCCCCCCCCCCCCCTCTTGCCCACCCTGAGCACTGCCCGGATC
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/clone_lib="NHH_MGC_44"
/lab_host="DH10B-R"
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Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
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AASPPLAETGAPRRFRRSVPRGEAAGAVQELARALAHLLEAERQERARAEAQEAEDOQ
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AAALRPRYVDDGPARPAQDEATDDVDPELLRYLLGRILAGSADSEGVAAPRRL
RRAADHDVGSELPPEGVLGALLRYKRLETPAPQVPARRLLPP"
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       /codon_start=1
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/protein_id="AAH02851.1"
/db_xref="GI:12804001"
                                                                                                          Length 993;
                                                                                                                           Indels
                                                                                                           ÷6
                                                                                                         Score 941.6; DB 9;
Pred. No. 4e-102;
; Mismatches 1;
                                                                                                                          5;
                                                                                                         Similarity 99.7%;
1; Conservative
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AAALRRPPVYDGGARGDAEAGDETPDVDPELLRYLLGRILAGRILAGRIAAGRAPPR
                                                                                                                                                                                                                                                                                                                                                                                                  Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalla; Butherla; Primates; Catarrhini; Hominidae; Homo.
1 (Dases I to 969)
Fricker,L., McKlnzie,A.A., Sun,J., Curran,E., Qian,Y., Yan,L.,
Patterson,S.D., Courchesne,P.L., Richards,B., Levin,N., Mzhavla,N.,
Devi,L.A. and Douglass,J.
                                                                                                                                                                                                                                                 PRI 27-JAN-2000
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Submitted (30-AUG-1999) Department of Molecular Pharmacology,
Albert Einstein College of Medicine, 1300 Morris Park Avenue,
Bronx, NY 10461, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              precursor"
AGTGCCCCCGCCATCCCGCCACCAGGACTGCTCCCGGCCAGCACGTCCAGAGCAACTTAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Identification and characterization of proSAAS, a granin-1
neuroendocrine peptide precursor that inhibits prohormone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Qian,Y., Ya
Levin,N., N
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/note="granin-like neuroendocrine peptide
/codon_start=1
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                                                                                                             CCGGCCAGCCAGCCTCTCACCCGAGGATCCCTACCCCTGGC
                                                                                        CCCGGCCAGCCACCCTCTCACCCGAGGATCCCTACCCCTGGC
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Pred. No. 6.2e-102;
4; Mismatches 4;
                                                                                                                                                                                                                                                                   proSAAS mRNA, complete cds
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J. Neurosci. 20 (2), 639-648 (2000)
20098938
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="FLHSAAS"
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                                                                                79.3%; Score 776.8; DB
.larity 99.7%; Pred. No. 1e-82;
Conservative 0; Mismatches
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                            /db_xref="taxon:9606"
297 c 201
   SAGAMI CHEMICAL RESEARCH CENTER
Location/Qualifters
1. 780
/organism="Homo sapiens
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Matches 778; Conserv
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AF181560
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ORIGIN
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TGCAGGAGCTGGCGGGGGCGCTGGCGCTGGTGGAGGCCGAACGTCAGGAGCGGGCGC
                                                                                                                                  CCGAGCTGTTGAGGTACTTGCTGGACGGATTCTTGCGGGAAGCGCGGACTCCGAGGGGG
                                                                                                   TGCAGGAGCTGGCGCGCGCGCGCGCATCTGCTGGAGGCCGAACGTCAGGAGCGGGCGC
                                                                                                                      TCTGGGGCGCCCCCCCCCAACTCTGATCCGGCTCTGGGCTTGGACGACGCCCCGACGCGC
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Catarrhini; Hominidae;
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proteins
Patent: WO 0112660-A 110 22-FEB-2001;
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Sequence 110 from Patent WO0112660.
AXO8418 G::13185255
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Mammalla; Eutheria; Primates;
1 (bases 1 to 780)
Kato,S. and Kimura,T.
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915 AGCACGICCAGAGCAACTIACCCCGGCCAGC 945
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AF181561
AF181561.1 GI:6653210
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /protein_id="AAF22641.1"
/dolxetein_id="AAF22641.1"
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APRRPRPVYDGPTGEPVEDAGDETPDVDPELLRYLLGRITGGSSEPEAAPARRLRR
SVDQDLGPEVVPDENVLGALLRVKRLENPSPQAPARRLLPP"
                                       1 (bases 1 to 1027)
Fricker, L., McKinzle, A.A., Sun, J., Curran, E., Qian, Y., Yan, L.,
Patterson, S.D., Courchesne, P.L., Richards, B., Levin, N., Mzhavla, N.,
Devi, L.A. and Douglass, J.
Identification and characterization of proSAAS, a granin-like
neuroendocrine peptide precursor that inhibits prohormone
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                           Sciurognathi; Muridae; Murinae; Mus
               Craniata; Vertebrata; Euteleostomi;
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/function="inhibits prohormone processing"
/functe="granin-like neuroendocrine peptide precursor"
/codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pred. No. 7.7e-62;
5; Mismatches 165; Indels 18;
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7.7e-62;
                                                                                                                                            Neurosci. 20 (2), 639-648 (2000)
                                                                                                                                                                                                                                                                                                                                     /organism="Mus musculus"
/db_xref="taxon:10090"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 599;
             Eukaryota; Metazoa; Chordata;
                           Mammalia; Eutheria; Rodentia;
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Location/Qualifiers
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ROD 27-JAN-2000 Ticker, L., McKinzie, A.A., Sun, J., Curran, E., Qian, Y., Yan, L., Partcker, D., Curchesne, P.L., Richards, B., Levin, N., Mzhavia, N., Devi, L.A. and Douglass, J. Levin, C. and Douglass, J. Gentification and characterization of proSAAS, a granin-like neuroendocrine peptide precursor that inhibits prohormone Ericker, L., McKinzie, A.A., Sun, J., Curran, E., Qian, Y., Yan, L., Patterson, S.D., Courcheene, P.L., Richards, B., Levin, N., Mzhavia, N., Devi, L.A. and Douglass, J.
Direct Submission
Submitted (30-AUG-1999) Department of Molecular Pharmacology, Albert Einstein College of Medicine, 1300 Morris Park Avenue, Rattus norvegicus Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; 99 674 720 780 794 840 854 434 614 675 CGCGGACTCCGAGGGGTGCCAGCCCCGCGCCCCCCCGCCGTGCCGCCGACCACGATGT 734 795 GACCCGGGGCCCCAGGTGCCTGCACGCCTCTTGCCACCCTGAGCACTGCCGGATC 427 Gececaecracacacacacaragescraracacaracacaracacacacaragesca 615 GACACCCGACGTGGACCCCGAGCTGTTGAGGTACTTGCTGGGACGGATTCTTGCGGGAAG 735 GGGCTCTGAGCTGCCCCCTGAGGGCGTGCTGGGGGGCGCTGCTGCGTGTGAAACGCCTAGA 841 GAACCCCTCGCCCCAGGCGCCGCCACGCCCCCTCCTGCCTCCTGAGCGCTG-CTGCATC 855 CCGTGCACCCTGGGACCCAGAAGTGCCCCCCCCCCCGCCACCACCAGGACTGCTCCCCGCC CGACGACCCCGACGCGCCTGCAGCGCAGCTCGCTCGCGCTCTGCTCCGCGCCCCGCCTTGA linear complete cds. mRNA processing J. Neurosci. 20 (2), 639-648 (2000)

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ROD 07-AUG-2002
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
1 (bases 1 to 975)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (06-AUG-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /codon_start=1
/product="Similar to granin-like neuroendocrine peptide
precursor"
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 /tissue_type="Colon, normal. 5 month old male mouse." /clone_lib="NCI_CGAP_Co24" /lab_host="DH10B"
                                                                                                             817 GCACGCCGCCTCTTGCCCACCCTGAGCACTGCCGGGATCCCGTGCACCCTGGGACCCAGAA 876
                                                                                                                                                                             877 GIGCCCCCGCCATCCCGCCACCAGGACTGCTCCCCGCCAGCACGTCCAGAGCAACTTACC 936
                                                                                                                                                                                                                                                                                                                                                                   Mus musculus, Similar to granin-like neuroendocrine peptide precursor, clone MGC:19107 IMAGE:4207854, mRNA, complete cds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  X., Hulyk, S.W., Hale, S.
S., Martin, R.G., Muzny,
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
CDNA Library Preparator Life Technologies, Inc.
CDNA Library Preparator Dr. The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Baylor College of Medicine Human Genome
                                               GGCGTGCTGGGGGGCTGCTGCGTGTGAAACGCCTAGAGACCCCGGGGCGCCCCAGGTGCCT
                                                                                                                                                                                                                                                                                                                                                         linear
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Center code: BCM-HGSC
Web site: http://www.hgsc.bcm.tmc.edu/cdna/
Contact: amg@bcm.tmc.edu
Gunaratne, P.H., Garcia, A.M., Lu, X., Huly
YCoon, V.S., Kowis, C.R., Lawrence, S., Mart
Richards, S., Gibbs, R.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Clone distribution: MGC clone distribution through the I.M.A.G.B. Consortium/ILNL at: Series: IRAK Plate: 24 ROW: p Column: 24. Location/Qualifiers
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20. .796
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AAALRPRPPVYDDGPTGPDVEDAADETPDVDPELLRYLLGRILTGSSEPEAAPAPRRL
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AASAPLAETSTPLRLRRAVPRGEAAGAVQELARALAHLLEAERQERARAEAQEAEDQQ
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                                                                               /.unction="inhibits prohormone processing"
/note="granin-like neuroendocrine peptide precursor"
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Pred. No. 6e-60;
1; Mismatches 205;
1. .945
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                                              clone-"FLRSAAS"
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RRASPRYPTFRPRAFPLAPDDDPDAFAAQLARALLRAKLDPAALGAQLVPAPA
PAPRPRPPVYDGGPHWPRRGCRRRDW"
                                                                                                                                                                                                                                                                                                Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                               highly basic protein,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 of Oral Medicine, National
Rockville Pike, Building 30
                                                                                                                                                                                                                                                                      Mis musculus

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleosto
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
1 (bases 1 to 1025)
Donadel,G., Marinos,N., Desilva,M.G., Lu,J., Notkins,A.L. and
Lan,M.S.

Molecular cloning and characterization of a highly basic prote
1R-4, expressed in pancreatic islets and brain
Neuroendocrinology 67 (3), 190-196 (1998)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Donadel, G., Notkins, A.L. and Lan, M.S.

Submitted (10-400-2000) Laboratory of Oral Medicine, Nation Institute of Dental Research, 9000 Rockville Pike, Building 124, Bethesda, MD 20892, USA

Location/Qualifiers

Torganism="Mus musculus" / Ab_xref="taxon:10090" / Ab_xre
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llarity 78.0%; Pred. No. 1.9e-50;
Conservative 5; Mismatches 173
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APRPRPPVLDGFTGPDVEDAGDETPDVDPELLRYLLGRILTGSSEPEAAPARRLRR
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                                                                                                                                                                                                                           18;
                                                                                                                                                                                 Length 975;
                                                                                                                                                                               Score 580.2; DB 10; Length
Pred. No. 1.3e-59;
0; Mismatches 163; Indels
                                                                                                                                                                               Match 59.3%;
Local Similarity 80.0%;
les 726; Conservative
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Best Local
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13.1	1.252 /evidence-not_experimental /fpt_family-*hlusx* 24. 356 /evidence-not_experimental /rpt_family-*hlusx* 397. 704 /evidence-not_experimental /rpt_family-*hlusy* // (rpt_family-*hlusy) // (rpt_family-*hlu	56495691 /evidence-not_experimental /rpt_danly="MIR" 613113747 /gene="GATA-1" /gene="GATA-1" /gene="GATA-1" /gene="GATA-binding protein 1" /product="GATA-binding protein 1" /note="mRNA acc. no. M30601"
CCTGGGCGCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC	repeat_region	repeat_region gene mRNA
CCTGGGCGCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC		
<ul><li></li></ul>	CTCAGGATCAGCAGGGGGGGGGGGGGGGGGGGGGGGGGG	5; 11106-52106: cosmid E2237; 27017-67034: 92644: cosmid D1425; 80573-113853: cosmid alifiers Homo sapiens" xxon:9606" -x; 9606" nids J1045; E2237; L1850; D1425; E1239"

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AC098339 62396 bp DNA linear HTG 24-AUG-2002 Rattus norvegicus clone CH230-2A16, *** SEQUENCING IN PROGRESS ***, AC098339
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   /note="homology = 75.00%, score = 24, counts
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                                               /rpt_unif=cactegrectgaacccacaaaggaa
complement(17629. .17940)
/rpt_dance=not_experimental
/rpt_fanily="MER33"
18028. .18353
/evidence=not_experimental
/rpt_fanily="MINII"
complement(18388. .18668)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      48.4%; Score 474.2; DB 9; llarity 99.4%; Pred. No. 6.9e-48; Conservative 0; Mismatches 3;
                                                                                                                                                                                                           /evidence=not_experimental
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19143. 19448
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/rpt_family="AluJb"
/wridence=not_experimental
/rpt_family="AluJb"
               /evidence=not_experimental
/rpt_type=tandem
                                                                                                                                                                                     /evidence=not_experimental
/rpt_family="Alusx"
complement(18674. .18977)
                                                                                                                                                                                                                                                                                                                                     /evidence=not_experimental
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                                                                                                                                                                                                                                                                                                                                                                 complement(20505. 20587)
/evidence=not_experimental
/rpt_family="MIR"
20598. 20658
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HTG; HTGS_PHASE1.
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Best Local Similarity
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Rearbaria. Adams, C., Adio-Oduola, B., All-osman, F. R., Allen, C., Alabrooks, S. L., Amaratunge, H. C., Are, J. R., Ayele, M., Banks, T., Barbaria. J., Benton, J., Blange, R., Blankenburg, K., Bondin, D., Burder, S., Elvera, M., Brown, E., Brown, M., Bryant, N. P., Burder, C., Burch, P., Bryant, N. C., Carron, T. F., Carrer, M., Cavazos, S. R., Chacko, J., Chavez, D., Carron, T. F., Carrer, M., Cavazos, S. R., Chacko, J., Chavez, D., Claveland, C.D., Cox.C., Coyle, M. D., Dathorne, S. R., David, R., Davila, M. C., Davy, Carroll, L., Dederich, D. A., Davila, M. Douthwaite, K. J., Dagar, D., Dathorne, S. R., David, R., Douthwaite, K. J., Dagar, D., Edgar, D., Edgar, D., Edgar, D., Edwards, C. C., Elbaj, C., Escotto, M., Falls, T., Ferraguto, D., Flagg, M., Ford, J., Foster, P., Frantz, P., Gabisi, A., Gao, J., Garner, H., Garner, T., Garza, M., Glll, R., Gabisi, A., Gao, J., Garner, M., Garner, P., Hande, S., Hamilton, K. J., Harris, C., Harris, K., Hart, M., Havlak, P., Hawes, A., Hernandez, O., Hodgson, A., Hogues, M., Holloway, C., Hollins, B., Homsi, F., Howard, S., Huber, J., Hully, S., Hume, J., Jackson, L. E., Jackson, L. E., Jackson, L. E., Jackson, L. E., Li, J., Li, Z., Lichtarge, O., Lieu, C., Liu, J., Liu, M., Loulse, H., Martindale, A., Martinez, E., Mahner, E., Mahner, E., Matchell, T., Mohabbat, K., Morgan, M., Morgan, M., Mapuer, E., McLedd, M., P., Liu, M., Martin, E., Mahner, G., Miner, Z., Mittchell, T., Workenkoo, S., Oguh, M., Okvennu, G., Oragunye, N., Orledo, R., Pater, M., Peeter, L., Peeter, L., Peeter, L., Peeter, S., Soctt, G., Shen, H., Shoshtari, N., Sison, I., Ruiz, S., Savery, G., Scherer, S., Soctt, G., Shen, H., Shoshtari, N., Sison, I., Tang, H., Ruiz, S., Savery, G., Sodergren, E., Soralke, T., Panker, A., Tanerisa, A., Tanerisa, M., Rolya, N., Rolyas, A., Rolybokan, T., Rolfe, M., Role, M., Rolyas, A., Rolybokan, T., Shoshtari, N., Stone, H., Tansey, J., Tanger, S., Wallliamson, A., Weiner, S., Weiner, S., Weiner, S., Weiner, Summission

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Submitted (24-AUG-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
On Aug 24, 2002 this sequence version replaced gi:21953722.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (23-OCT-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA (bases 1 to 62396)
                     Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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Sequencing vector: Plasmid;
Chemistry: Dye-terminator Big Dye: 100% of reads
Assembly program: Phrap; version 0.990329
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Center code: BCM
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------- Project Information
Center project name: TULN
Center clone name: CH230-2A16
                                                                                                                    (bases 1 to 62396)
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NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
NOTE: This is a 'working draft' sequence. It currently consists of 38 contigs. The true order of the places is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
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Worley, K.C.

Direct Submission

Baylor Diaza, Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

Gases I to 77876)

Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequencing vector: Plasmid;
Chemistry: Dye-terminator Big Dye: 100% of reads
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Consensus quality: 42256 bases at least Q40
Consensus quality: 47276 bases at least Q30
Consensus quality: 50269 bases at least Q30
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Contact: hgsc-help@bcm.tmc.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Center: Baylor College of Medicine
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
NOTE: This is a "working draft' sequence. It currently consists of 36 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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*** SEQUENCING IN PROGRESS ***,
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Rattus norvegicus
Bukatyota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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Muzny, D.M., Adams.C., Adio-Oduola,B., Ali-osman,F.R., Allen,C.,
Alsbrooks,S.L., Adamstaunge,H.C., Are,J.R., Ayele,M., Banks,T.,
Barbaria,J., Benton,J., Bimage,K., Blankenburg,K., Bonnin,D.,
Bouck,J., Bowle,S., Brieva,M., Brown,E., Brown,M., Bryant,N.P.,
Buhay,C., Burch,P., Burkett,C., Burrell,K.L., Byd.N.C.,
Carron,T.F., Carter,M., Cavazos,S.R., Chacko,J., Chavez,D.,
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Pred. No. 2.1e-32;
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/organism="Rattus norvegicus"
/db_xref="taxon:10116"
/clone="CH230-2423"
17600 c 17320 g 19098 t
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Cleveland, C.D., Cox, C., Coyle, M.D., Dathorne, S. R., David, R.,
Davila, M.L., Davis, C., Coyle, M.D., Dathorne, S. R., David, R.,
Davila, M.L., Davis, C., Davy-Carroll, L., Ding, Y., Dinh, H. H.,
Douthwaite, K.J., Dragaro, O., Dam, A.L., Ding, Y., Dinh, H. H.,
Douthwaite, C., Edgar, D., Edgards, C. C., Elhaj, C., Escotto, M.,
Earnhart, C., Edgar, D., Flagg, N., Ford, J., Foster, P., Frantz, P.,
Gabisl, A., Gao, J., Garcia, A., Garner, Y., Garza, N., Gill, R.,
Gorrell, J. H., Guevara, W., Ganner, P., Habe, S., Hamilton, K.,
Harris, C., Hadris, K., Hart, M., Havlak, P., Hawes, A., Hernandez, J.,
Hernandez, O., Hodgson, A., Houges, M., Holloway, C., Hollins, B.,
Jacobson, B., Jak, Y., Johnson, R., Johlwet, S., Jouchs, S.,
Jacobson, B., Lichtarge, O., Liud, T., Korvah, J., Kovar, C.,
Li, J., Li, L., Lichtarge, O., Liud, C., Liul, M., Loulseged, H.,
Lozado, R., Lichtarge, O., Liud, C., Liul, M., Loulseged, H.,
Lozado, R., Lichtarge, O., Liud, C., Liul, J., Liul, W., Loulseged, H.,
Lozado, R., Lichtarge, O., Liud, C., Liul, J., Liul, W., Loulseged, H.,
Lozado, R., Lichtarge, O., Liud, C., Liul, J., Martinez, E.,
Mansehwari, M., Mapua, P., Martin, R., Martindale, A., Martinez, E.,
Marsey, E., Manniney, E., McLeod, M. P., Meador, M., Morris, S.,
Miner, G., Minch, Z., Mitchell, T., Mohabbat, K., Morgan, M.,
Novierson, E., Newtson, J., Newtson, N., Nguyen, N., Nickerson, E., Nwokenko, S., Oguh, M., Okwuon, G.,
Scherer, S., Scott, G., Shen, H., Shoosheari, N., Sisson, I.,
Sucton, A., Svatek, A., Tabor, P., Tamerisa, A., Tamerisa, K.,
Tansey, J., Taylor, C., Taylor, P., Tamerisa, A., Tamerisa, K.,
Wulliams, G., Milliamson, A., Wleczyk, R., Wooden, S., Warley, W.,
M., Whyen, W., Wulliamson, A., Wleczyk, R., Neoden, S., Warley, W.,
Wulliams, G., Williamson, A., Wleczyk, R., Wooden, S., Warley, W.,
Wulliams, G., Walliamson, A., Wleczyk, R., Wooden, S., Warley, W.,
Wulliams, G., Walliamson, A., Wleczyk, R., Wooden, S., Warley, W.,
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NOTE: This is a 'working draft' sequence. It currently consists of 53 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (15-SEP-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA (bases I to 111948) Worley, K.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (11-JUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
On Jul 10, 2002 this sequence version replaced gi:17941324.
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Contact: hgsc-help@bcm.tmc.edu
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Direct Submission

Submitted (13-MAY-2002) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 15A, UK. E-mail enquiries:

Umquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On May 25, 2002 this sequence version replaced gi:21104114.

During sequence assembly data is compared from overlapping clones.

Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >-30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one MI3 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em:, EMBL; Sw:, SWISSRROT; Tr:, TREMBL; WP:, MORMPEP; Information on the WORWPEP than their feature fails and with their source databases: Em:, EMBL; Sw:, Anderson on the WORWPEP.
                                                                      ROD 23-MAY-2002
                                                                   AL670169 151694 bp DNA linear ROD 23-MAY-200:
Mouse DNA sequence from clone RP23-198C2 on chromosome X, complete
                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             http://www.sanger.ac.uk/Projects/C_elegans/wormpep RP23-198C2 is from the RPCI-23 Mouse PAC Library constructed by the group of Pieter de Jong. For further details see http://www.chori.org/bacpac/home.htm
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Muzny, D.M., Adams, C., Addo-Odduola, B., Ali-Osman, F.R., Allen, C., Alabrooks, S.L., Amaratunge, H.C., Are, J.R., Agele, M., Banks, T., Alabrooks, S.L., Amaratunge, H.C., Are, J.R., Agele, M., Banks, T., Barban, C., Burch, S., Bartera, M., Brown, E., Brown, M., Bryant, N.P., Burbar, S., Burch, S., Bartera, M., Brown, E., Brown, M., Bryant, N.P., Burbar, C., Burch, F., Burkett, C., Burth, E., Byrd, N.C., Carten, G., Chen, S.R., Chacko, J., Chavez, D., Clee, and C.D., Carten, M., Day, Cartell, K.L., Byrd, N.C., Coyle, Cartell, M.C., Day, Cartell, D. Bartla, M.L., Davis, C., Coyle, M.D., Dathorne, S.R., David, R., Day, Cartell, D. Bartla, M.L., Davis, C., Coyle, M.D., Dann, A.L., Ding, Y., Dinh, H. H., Douthwaite, K. J., Draper, H., Dugan-Rocha, S., Durbin, K.J., Earnbart, C., Edgar, D., Edwards, C.C., Elhaj, C., Escetch, F. Frantz, P. Gabisi, A., Gao, J., Garcia, A., Garca, M., Gall, R., Marliton, K., Harris, C., Houle, S., Huber, J., Holyer, S., Hale, S., Hale
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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Rattus norvegicus
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KEYWORDS
SOURCE
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Morley, K.C.

Direct Submission
Submitted (26-MAY-2002) Human Genome Sequencing Center, Department Submitted (26-MAY-2002) Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 177613)
Worley, K.C.

Worley, K.C.
Submission
Submitted (24-JUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

Baylor Plaza, Houston, TX 77030, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
NOTE: This is a "working draft' sequence. It currently consists of 63 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as arbitrary. Gaps between the contigs are represented as This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
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Direct Submission
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Horrigan, S., Soppet, D.R. and Weaver, Z.
Cancer gene determination and therapeutic screening using signature
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Avalon Pharmaceuticals (US)
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